

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 22:27:32 ; Search time 44 Seconds

(without alignments)
1431.942 Million cell updates/sec

Title: US-10-663-157-2

Perfect score: 3456

Sequence: 1 MGNSPSSSTALASCRIARR.....SQEASQTLDSVYSHLPDLL 655

Scoring table: BLOSSOM62

Gapop 10.0 , Gapext 0.5

Searched: 28336 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 28336

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : PIR-78:*

1: Bir1:*

2: Bir2:*

3: Bir3:*

4: Bir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2350	68.0	651	2	JC7705	death receptor-6 -
2	235.5	9.9	461	1	A35356	tumor necrosis fac
3	235.5	8.0	459	2	I49854	gene murine tumour
4	213.5	7.9	474	2	B38634	tumor necrosis fac
5	235.5	6.8	416	1	JN0006	nerve growth facto
6	235.5	6.8	255	2	I38426	lymphocyte activat
7	223.3	6.7	305	2	A46476	B cell-associated
8	223.3	6.6	435	2	I41482	tumor necrosis fac
9	218.5	6.3	326	1	GQY2ML	T2 protein - myxom
10	211.5	6.1	325	2	B13692	T2 protein - rabbi
11	211.5	6.1	425	1	A26431	nerve growth facto
12	210.0	6.1	427	1	GOHUN	nerve growth facto
13	206.5	6.0	348	2	T28623	hypothetical prote
14	206.5	6.0	349	2	D36858	gene G4R protein -
15	205	5.9	595	2	A42086	CD30 antigen precu
16	204.5	5.9	349	2	D72175	G2R protein - vari
17	200	5.8	277	2	A60771	B-cell activation
18	193	5.6	461	2	JC4302	tumor necrosis fac
19	191.5	5.5	2824	2	T22759	hypothetical prote
20	187.5	5.4	493	2	JC5486	membrane glycoprot
21	186.5	5.4	461	1	GQRTT1	tumor necrosis fac
22	180.5	5.2	256	2	B32393	T-cell antigen 4-1
23	170	4.9	454	1	QGMST1	tumor necrosis fac
24	154	4.5	277	2	I37552	OX40 homolog - hum
25	148	4.3	271	2	S2783	OX40 antigen precu
26	145	4.2	455	2	GQHUT1	tumor necrosis fac
27	142.5	4.1	1193	2	A4018	laminin B2 chain
28	138	4.0	1827	2	T34288	hypothetical prote
29	136.5	3.9	1205	2	T27053	hypothetical prote

RESULT 1

JC7705

death receptor-6 - chicken

C;Species: Gallus gallus (chicken)

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 07-Jul-2003

C;Accession: JC7705

R;Bridgeman, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.

Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001

A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.

A;Reference number: JC7705; PMID:21308433; MUID:11414698

A;Accession: JC7705

A;Molecule type: mRNA

A;Residues: 1-651

A;Cross-references: GB:AF349908

C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs to the TNF receptor superfamily and activates a cell death and/or survival signaling cascade.

C;Genetics:

A;Gene: dr-6

C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C;Keywords: ovary

F;1-21/Domain: signal sequence #status predicted <SIG>

F;12-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>

F;32-390/Domain: transmembrane #status predicted <TM>

F;10-415/Domain: death domain #status predicted <DBD>

F;551-651/Region: conserved cytoplasmic #status predicted

Query Match 68.0% ; Score 2350; DB 2; Length 651;
Best Local Similarity 70.6% ; Pred. No. 5..8e-148;
Matches 46; Conservative 47; Mismatches 102; Indels 46; Gaps 10;

Qy 23 ATMAGSLILLGLFTSTTQAQP-----EOKASNLL-IGTYRHYDRTGQVLTCDKPCAGTVYVS 77

Db 3 AAVIAVLLPLLLGTTADAQPLKLTSEQNAVSLPAGKYLHLDRAATNQPLICDKPCAGTVYVS 62

Qy 78 EHCTNTSLRVCCSSCPGFTTRHENGTEKCHDCSQCPWPMEKLPKAALTDECTCPGM 137

Db 63 KHCYKSTLRECSPPDGFTKENGIBRCHPCPKLMEKTHCTALTDECTCLSGT 122

Qy 138 FQSMATCAPIHTCPVPGKRCARTEFSDYPSYSMKCKRAVTDCLSQLN 197

Db 123 FQNDTCVPTVCPVGWVGRKKGTETEVRCPKLRTEFSDYPSYSMKCKTVDCEGRNM 182

Qy 198 VVTKPGTKETDNC---GTLP-- SFSSSSTSPPSPASLNTSITSSDAQDG-----ETYBAPPTAYLPGLN 232

Db 183 VVVKPGTKESDNTYCXSPASLNTSITSSDAQDG-----ETYBAPPTAYLPGLN 232

Qy 253 STEENSSASVRPKLSSSQEGTVDNTSSARGKEDVNTLPLQVNVHQGPHRHFLKL 312

Db 233 SSVFDSLSSSPAPRVNSGTAPEIYDNTISANGTVAQPSLSSAGTQAOQSYRKHTSQA 292

Qy 313 L---PSMEATGGKSSSTIKGPGRGHPRQLKHFDFNEHLPMMIVFLLVLVIVTCVS 369

ALIGNMENTS

A;Residues: 1-22 <KIS>	Q;Cross-references: ENB1:XB7128; NID:9809043; PIDN:CAA6618-1; PID:9809044
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog	C;Keywords: cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>	C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
F;23-474/Domain: tumor necrosis factor receptor type 2 #status predicted <MAT>	C;Comment: The cytosine-rich region of the extracellular domain may form part or all of
F;40-77/Domain: NGF receptor repeat homology <NG1>	C;Comment: This protein is thought to form a high-affinity receptor when it associates
F;79-120/Domain: NGF receptor repeat homology <NG2>	C;Superfamily: nerve growth factor receptor: NGF receptor repeat homology
F;166-203/Domain: NGF receptor repeat homology <NG4>	C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
Query Match	Best Local Similarity 7.9%; Score 273.5; DB 2; Length 474;
Matches 82; Local Similarity 25.0%; Pred. No. 1.5-10;	Matches 34; Mismatches 127; Indels 85; Gaps 10;
Qy 65 LRDKXCPATYVSEPHCTNTSLRVYSSCPVNGTFRPHENGIBKCHADCSQPCPWPMLIEKLPPA 124	Db 53 MCAAAXKCPQQYXRFCNKNTSDTCADEASMYQVQANQFRTCLSCSSSTTDQVEIRAT 112
Qy 113 KQONRVCACEAAGRCAKTHSGSCQCMRSLSKPGFQYASSRAPNGNVLCKACAGTFS 172	Db 178 DVPSSVMKCKAYTDCDLSONLVVVKIKGPTKETDNYCGTLPSSPSGTCATAIPPRPHME 237
Qy 173 DRTSTDVQEPHRIC---SILAKPGNASTDAVCA-----PESPT 208	Db 209 LSAIPRTLYVSSQPPTRSPQPLDQEPGPSCQTPSILSL-GSTPIEQSTKG---GISPAT 262
Qy 238 THEYPSSTV---PKGMNSTEENSSASVRPKVLISSIQEGTVPDNTSSARGKEDVNKNLIP 293	Db 294 -----NLQVN-----HQGPH-----HRHILK 311
Qy 263 IGLIVGVTSLGLMLGLYNCITLIVRKKEPKSCLQRDARYPHVDEKSQDAVGLEQQHILT 322	Db 312 LIPPMEAATGEKSTT--PLKGPRGRHPR 337
Qy 323 TAPSSSSLESSASAGDRRAPPGHPO 350	Db 323 TAPSSSSLESSASAGDRRAPPGHPO 350
RESULT 5	
UN0006	nerve growth factor receptor, low affinity precursor - chicken
N;Alternative names: NGF receptor	C;Species: Gallus gallus (chicken)
C;Accession: 10-Sep-1999 #sequence_change 10-Sep-1999	C;Accession: 10-Sep-1999 #sequence_change 10-Sep-1999
R;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reis	R;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reis
A;Title: Structure and developmental expression of the nerve growth factor receptor in	C;Superfamily: nerve growth factor receptor: NGF receptor repeat homology
A;Reference number: UN0006; MUID:90166579; PMID:2560385	C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
A;Accession: UN0006	F;1-20/Domain: signal sequence #status predicted <SIG>
A;Molecule type: mRNA	F;21-416/Domain: nerve growth factor receptor #status predicted <MAT>
A;Residues: 1-416 <LAR>	F;21-239/Domain: extracellular #status predicted <EXT>
A;Experimental source: embryonic chick brain	F;24-575/Domain: NGF receptor repeat homology <NG1>
R;Reuer, J.G.; Fatemie-Nairine, S.; Wheeler, E.F.; Bothwell, M.	F;49-100/Domain: NGF receptor repeat homology <NG2>
Dev. Biol. 137: 287-304, 1990	F;101-159/Domain: NGF receptor repeat homology <NG3>
A;Title: Structure and developmental expression of the chicken NGF receptor.	
A;Accession number: A60504	
A;Accession: A60504	
A;Status: preliminary; not compared with conceptual translation	
A;Molecule type: mRNA	
A;Residues: 21-35, 'Y', 37-112, 'K', 174-275, 'S', 277-395, 'R', 397-416 <HEU>	

RESULT 8

15182 tumor necrosis factor receptor 2-related protein - human
 C:Species: Homo sapiens (man)
 C:Accession: I54182
 R:Baens, M.; Chaffner, M.; Cassiman, J.J.; van den Berghe, H.; Marynen, P.
 Genomics 16, 114-118, 1993
 A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequences
 A:Accession: I54182; MUID:93252381; PMID:8463660
 A:Cross-references: GB:154182; OMIM:600979
 A:Gene: GDB:LTBR
 A:Cross-references: GDB:1230195; OMIM:600979
 A:Map Position: 12p13.3-12p13.1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 Query Match 6.6%; Score 228.5; DB 2; Length 435;
 Best Local Similarity 30.9%; Pred. No. 1.3e-07;
 Matches 56; Conservative 23; Mismatches 65; Indels 37; Gaps 8;

Db 65 LTCDKCPAGTYSEHCTNTSLRVCSSPVGTFTRHENGIEKHDGSCOPC-PWPMIEKL-P 122
 57 ICGSRCPGTYSAKCSRIRDTCATAGNSNEHYNLTCQLC-RPCDVMGIEEIAPIP 115

Qy 123 CAAITDRECTCPGGMFQSNTACAPHTY------CPVGWGVKKKGTERB----- 164
 Db 116 CTSKRKTQCRGCGMF-----CRAWALECTHCELLSSCP-----PGTEAKLDEVGKG 163

Qy 165 DVCKQCARGFSDVPSVVMKCKAYTQLSQNIVVKGTEIDNNGT-----LSPSSSS 220
 Db 164 NNHCVPCKAGHENTSSPSARCQPHTRCENQSLVERAAGTAQSDTICKNPLEPMSG 223

Qy 221 T 221
 Db 224 T 224

RESULT 9

GQVZML

15182 t2 protein - myxoma virus (strain Lausanne)
 C:Species: myxoma virus
 C:Accession: I54182
 R:Upton, C.; Macen, J. L.; Schreiber, M.; Mcfadden, G.
 Virology 184, 370-382, 1991
 A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor receptor
 A:Reference number: A40566; MUID:91335768; PMID:1651597
 A:Accession: A40566
 A:Molecule type: DNA
 A:Cross-references: GB:M95181; PID:93323309; PID:AAA46632.1; PMID:9332310
 C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology
 R:64-147/Domain: NGF receptor repeat homology <NG3>
 R:66-181,205-238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.3%; Score 218.5; DB 1; Length 326;
 Best Local Similarity 36.8%; Pred. No. 4.2e-07;
 Matches 50; Conservative 10; Mismatches 69; Indels 7; Gaps 2;

Qy 65 LTCDKCPAGTYSEHCTNTSLRVCSSPVGTFTRHENGIEKHDGSCOPC-PWPMIEKLPCA 124
 Db 38 LCCTSCCPGTSASRLCCPGSDTVCSPKNEFTASTMADAVCVSQRGRTGHLSPSQSCD 97

Qy 125 ALTDRECTCPGMF-----QSNATCAPIHTCPGVGMGVRKKGTETEDVRCKQCARGTFS 178
 Db 98 RTHDRVCNCSTGNMCLLKQNGCERIACQTKPHTCEKCPHFTSD 156

Qy 179 VPSSYMKC 186
 Db 157 SLSPERC 164

RESULT 10

B43692 T2 protein - rabbit fibroma virus
 C:Species: rabbit fibroma virus, Shope fibroma virus
 C:Accession: B43692
 R:Upton, C.; DeLand, A.M.; McFadden, G.
 Virology 160, 20-30, 1987
 A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric A;Reference number: A43692; PMID:87321103; PMID:2820128
 A:Accession: B43692
 A:Cross-references: GB:17433
 C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology <NG2>
 F:64-105/Domain: NGF receptor repeat homology <NG3>
 F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 6.1%; Score 211.5; DB 2; Length 325;
 Best Local Similarity 36.7%; Pred. No. 1.2e-06;
 Matches 47; Conservative 7; Mismatches 67; Indels 7; Gaps 2;

Qy 65 LTCDKCPAGTYSEHCTNTSLRVSSCPVGTFTRHENGIEKHDGSCOPC-PWPMIEKLPCA 124
 Db 38 LCCTSCCPGTSASRLCCPGSDTVCSPKNEFTASTMADAVCVSQRGRTGHLSPSQSCD 97

Qy 125 ALTDRECTCPGMF-----QSNATCAPIHTCPGVGMGVRKKGTETEDVRCKQCARGTFS 178
 Db 98 RTHDRVCNCSTGNMCLLKQNGCERIACQTKPHTCEKCPHFTSD 156

Qy 179 VPSSYMKC 186
 Db 157 SLSPERC 164

RESULT 11

A2631

nerve growth factor receptor precursor, low affinity - rat
 N:Alternative names: NGF receptor
 C:Species: Rattus norvegicus (Norway rat)
 C:Accession: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Cross-references: GB:X05137; PID:956755; PID:CAA28783.1; PID:956756
 R:Radeke, M. J.; Masko, T. P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
 Nature 325, 593-597, 1987
 A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
 A:Reference number: A26431; PMID:87115859; PMID:3027580
 A:Accession: A26431
 A:Molecule type: mRNA
 A:Cross-references: 1-425 <RAD>
 R:Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Person, H.
 Gene 121, 247-254, 1992
 A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoic acid
 A:Reference number: PH1229; PMID:1446821
 A:Accession: PH1229
 A:Molecule type: DNA
 A:Cross-references: GB:X61269
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
 C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
 C:Comment: This protein is thought to form a high-affinity receptor when it associates
 C:Genetics:
 A:Introns: 20/3
 C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C; Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; protein; signal sequence #status predicted <SIG>
 P; 10-425/Product: nerve growth factor receptor #status predicted <MAT>
 P; 30-251/Domain: extracellular #status predicted <EXT>
 P; 33-66/Domain: NGF receptor repeat homology <NG1>
 P; 68-109/Domain: NGF receptor repeat homology <NG2>
 P; 110-148/Domain: NGF receptor repeat homology <NG3>
 P; 150-190/Domain: NGF receptor repeat homology <NG4>
 P; 198-249/Region: serine/threonine-rich
 P; 252-273/Domain: transmembrane #status predicted <MEM>
 P; 274-425/Domain: intracellular #status predicted <INT>
 P; 61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 211.5; DB 1; Length 425;
 Best Local Similarity 22.3%; Pred. No. 1.7e-06;
 Matches 119; Conservative 59; Mismatches 196; Indels 145; Gaps 25;

Qy 112 ACSRRIRATATMIGSLLGLFLTTAQEQAASNLIGLTYRHDRAVQVLTCDKCP 71
 Db 6 AACSAMDRL-----RLLLILGYSGGAKCST - GLYTH --SGB - CCKAGN 49

Qy 72 AGTYVSEHCTNTSLRVCCSPCGV-TFTRHENGIEKHDSCSOPCPKPMIXLPCAAALTDE 130
 Db 50 LGFGVAQG-C-GAQTEVBPCLDNVT-SDVVSATEPKPKTE - CLELQMSHASPCTEADDV 107

Qy 131 CTCPPGMNQSNAT - CAPHTYCPVGNGVRKGKTETEDVRCCKOCARGTFFSDPVSSYMKCKA 188
 Db 108 CTCAGYQDDEBTGHCACSVCEVQGLVFSQCDKNTVCEBPCGTYCSTGTTT 167

Qy 189 YFDQLSNQNLUVVVKPGIKEETDNGCTLPSSSSTSPSPGTAIPPRDEHMETHEVPSSTYF 248
 Db 168 CTCV-C-EDTEROLRECTPWADABCEELFG-----RWPIRST-PP 203

Qy 249 KGMNST-ESNSSANASVRPKVLSLQEGTVPDNTTSAEGKDVKNTLDPNQVNHHQGPCHR 307
 Db 204 ESSDSTAESTQEBEVPE - QDLPVSPYADYTTW----- 238

Qy 308 HILKLKPMEATCGEKSSTPIKGPKRSHPRONLHKHFDINHFLPMMIVFLLLVIVTV 367
 Db 239 -----SSQPV - -VTRG-TTDNL-----IP - VYCSILAAUVVGLY 268

Qy 368 CSTR---KSSRTLKKGRQDPSATVEKAGLKKSMPTONREKWTYYCNGHGDILKLYA 423
 Db 269 ATIAFKGWNNSCKNQGANSRP-----VQDQPPPEBK - LHSQGTSVDSQSLHD 317

Qy 424 AQYGSQWK-----DIYQELCNASREVAFAFSNGYTAH - -ERAY----- 460
 Db 318 QOHTCOPASQOALKGDNLYSSPLTKEVKKLNGDTWHLGAGLGYQPEHIDSFTHE 377

Qy 461 -----AALQHWTTRGPBASLAQALISALQRHRNDVYKEI 494
 Db 378 ACPVRAALLASWGRQ-DSATLDAALLAARRQADIVESTL 415

RESULT 12
 nerve growth factor receptor precursor, low affinity (validated) - human
 C; Alternative names: NGF receptor
 C; Species: Homo sapiens (man)
 C; Accession: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-2000
 R; Johnson, D.; Lanahan, A.; Buch, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
 Cell 47, 545-554, 1986
 A; Title: Expression and structure of the human NGF receptor.
 A; Reference number: A25218; MUID:87051722; PMID:3022937
 A; Accession: A25218
 A; Molecular type: mRNA
 A; Residues: 1-427 <J0H>
 A; Cross-references: GB:M14764; NID:G-89204; PID:AB59544-1; PID:9189205
 R; Diezschold, B.; Barley Jr., J.J.; Schatterman, G.; Thompson, S.; Grob, P.;
 J. Neurochem. 48, 225-232, 1987
 A; Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
 A; Reference number: A60204; MUID:8705574; PMID:3035363

A; Accession: A60204
 A; Molecule type: protein
 A; Residues: 29-107, 'T', '33-42, 'T', '45-46, 'T', '50-51, 'XX', '54-56 <MAR>
 A; Experimental source: melanoma cell line AB55
 A; Note: this sequence has been corrected by a note added in proof to follow the nucleotides 30-251/Domain: extracellular #status predicted <EXT>
 R; Visvajjhala, P.; Leszyk, J.D.; Lin-Boerke, J.; Ross, A.H.
 Arch. Biochem. Biophys. 294, 244-252, 1992
 A; Title: Structural domains of the extracellular domain of human nerve growth factor receptor
 A; Reference number: S21689; MUID:9198071; PMID:1372492
 A; Accession: S21689
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 183-208 <VIS>
 R; Sehgal, A.; Patel, N.; Chao, M.
 Mol. Cell. Biol. 8, 3160-3167, 1988
 A; Title: A constitutive promoter directs expression of the nerve growth factor receptor
 A; Reference number: 157638; MUID:8309693; PMID:250481
 A; Accession: 157638
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-22 <RES>
 A; Cross-references: GB:M21621; NID:9189206; PID:AAA36363-1; PID:g189207
 C; Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells. The cysteine-rich region of the extracellular domain may form part or all of the receptor. This protein is thought to form a high-affinity receptor when it associates with the nerve growth factor receptor.

C; Comment: This receptor undergoes both N- and O-linked glycosylation.

C; Genetics:
 A; Gene: GDB:NGFR
 A; Cross-references: GDB:120234; OMIM:162010
 A; Map Position: 17q21-17q22
 C; Superfamily: nerve growth factor receptor; NGF receptor repeat homology
 C; Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; transmembrane
 P; 1-28/Domain: signal sequence #status Predicted <SIG>
 P; 29-427/Domain: nerve growth factor receptor #status experimental <MAT>
 P; 29-250/Domain: extracellular #status Predicted <EXT>
 P; 32-65/Domain: NGF receptor repeat homology <NG1>
 P; 67-108/Domain: NGF receptor repeat homology <NG2>
 P; 109-147/Domain: NGF receptor repeat homology <NG3>
 P; 149-189/Domain: NGF receptor repeat homology <NG4>
 P; 197-248/Region: serine/threonine-rich
 P; 51-272/Domain: transmembrane #status Predicted <TRM>
 P; 273-427/Domain: intracellular #status Predicted <INT>
 P; 60/Binding site: carbohydrate (Asn) (covalent) #status Predicted

Query Match Score 210.5; DB 1; Length 427;
 Best Local Similarity 22.8%; Pred. No. 2e-06;
 Matches 116; Conservative 58; Mismatches 204; Indels 131; Gaps 22;

Qy 21 ATATMIASSLIGLFLETTAPEQKASNLIGTYRVRDAGQVLTCDKCPAGTYVSEHC 80
 Db 5 ATGRAMDCPRLLILGVLGSLLGAKEACP-TGLYTH----SGE---CCKACNIGEGAQPC 57

Qy 81 TNTSLRVSSC-PVGTGTRHENGIEKHDSCSQCPWPMIEKLPICALTDRECTCPGMFQ 139
 Db 58 -GAGQNTVEPCLDSVTSATEPKPCTE-CVQLOSMAPCVFADDAVCARYYYQ 115

Qy 140 SNAT-CAPHTYCPVGNGVRKGKTETEDVRCQKOCARCTFDVPSYSYMKCKAYTDCLSQLN 197
 Db 116 DEITGRCEACRVEGAGSGLVFSQDKDNTVCECPDGTCLCPCV-EDTE 174

Qy 198 VVTKPGKTEIDNC-----GTPSFSSSTSSPGTATEPREHMETHEVPSSTYV 247
 Db 175 ROLRECWRWADACCEIFGRWTRSTPPEGSDTAPB----QBPPAPPQDLAISTVA 229

Qy 248 PKGMNSTBGSNSASVRPK-----VLISSQBGTVPDNTSSARGKEDDVNKTLPNL 295
 Db 230 -GIVTTGNGSSQPVTRGTTDNLIPYCSILAAVYGLVYIAFKRWNSCQNKOGANS 287

Qy 296 QVNNHQQGPBHRHILKLLPSMEATGGEK - SSTPIKSPKRGHPRQNLHKHFDINELPWN 353
 Db 286 RPNTQTPPE-----GEKLHSDGSIYSDS----QSLH---DQCPH--- 320

Qy 354 IVLFLLIVVIVVCSIRKSSRLTKGPRQDPSAIVRAGLKKSMPTQNREKIVIYCNG 413

Qy 139 QSNATCAPIHTVCPVGVGTVKKCTETEDV-----RCKOCARGTF----- 176
 Db 120 NSCARCPIPHSVCAGMTVKFGRQAQNTVCEBASPGVSPACASPIENCKEBSGTIPQAKP 179
 Qy 177 -----SDPESV----- 183
 Db 180 TPVSPATSSASTMPVRGGTRLQAEEAASKLTRAPDPSVGRSSSDPGLSPTQPCPGSD 239
 Qy 184 -----MKCAYTDDLSQNLIVIKPGTETDNYCGLPSFSSTSPSGTA- 228
 Db 240 CRKQCEPPDYLDEAGRCYAC/CSRDLLVEKTPCARNSSRICECRPGMCAATNSCAR 295
 Qy 229 IFPRPERMETHEVPSSTVPKGMNSTSNSASVRPKVLSI1QEGTVPDNTSSARGKEDV 288
 Db 300 CVPPY-----ICAETVTRPQDMAEKDTPEAP-----GTQPDNPPTPENGEAP 345
 Qy 289 NKTEPNLQYVNHQGPHRHRHILKLPMSMEATGEGKSSTPKGPKRGHPRQNLHKHFDINE 348
 Db 346 ASTSPPTQCLLVDQSAS-----KTLPT-----PTSAVALLSTCKP-----VLDAGP 386
 Qy 349 HPPWMIVFLLYVWVY-----YCSIRKSSRTLKG-----PRQDPSAIVEKAGLKKS 397
 Db 387 VLFWVI-----LYLWVYVGGSAFLLCRACKRKRQKLHLCYPTQSQPKLEYDSDRPR 441
 Qy 398 MFTQNQRKWIYQCNHGIDIKLVAQVGSQWQDLYQFLCNASEREVAAFNSNGYTADE 457
 Db 442 RSSTQLS-----GASVTEPVAAERGLMSQPLME-TG-----HS 474
 Qy 458 RAYAALQWTIR-----GPEASLAQIISARCRHRINDVYEKIRGIMEDDTQLETTDKLAL 511
 Db 475 VGRAYLESPLQDASPGPSSPRDLPEPRVSTEHNTNKEKYMKADETVIGTVKAEL 534
 Qy 512 PMSPSPSPSPSPNARLSENSALLTVEPSQDKNGFYDESEPL 558
 Db 535 PEGRGLAGPAA-PELESELE-----ADHTPHYPEQETEPL 569

Search completed: September 21, 2004, 22:41:15
 Job time : 46 secs

RESULT 2
US-09-314-844F-2

Sequence 2, Application US/09314844F
Patent No. 6660839
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH CHARLES
APPLICANT: HURLE, MARK R.
APPLICANT: YOUNG, PETER
APPLICANT: TAN, K. B.
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED
CURENT APPLICATION NUMBER: US/09/314, 844F
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 60/041,796
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: US 08/959,382
PRIOR FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 2
LENGTH: 655
TYPE: cDNA
ORGANISM: HOMO SAPIENS
US-09-314-844F-2

RESULT 3
US-09-756-854-2
Sequence 2, Application US/09756854
Patent No. 6667390
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
Fan, Ping
Gent, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3.0
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 655 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: Protein

241 VPSSTVPGMNSTEENSSAVRPVLSIQBGTYPDNTSSARGEDVNTKLPNLIQVNNH 300
Qy 241 VPSSTVPGMNSTEENSSAVRPVLSIQBGTYPDNTSSARGEDVNTKLPNLIQVNNH 300
Db 241 VPSSTVPGMNSTEENSSAVRPVLSIQBGTYPDNTSSARGEDVNTKLPNLIQVNNH 300
Qy 301 QGGPHRHILKLLPSMEATGEGKSSTPIKGPKRGHRPQNLHKHFDINEHLPWMTLFLLL 360
Db 301 QGGPHRHILKLLPSMEATGEGKSSTPIKGPKRGHRPQNLHKHFDINEHLPWMTLFLLL 360
Qy 301 QGGPHRHILKLLPSMEATGEGKSSTPIKGPKRGHRPQNLHKHFDINEHLPWMTLFLLL 360
Db 301 QGGPHRHILKLLPSMEATGEGKSSTPIKGPKRGHRPQNLHKHFDINEHLPWMTLFLLL 360
Qy 361 VLVVIVVCSIRKSSRTLKGKPRQDPSAIVEAGLKLKSMTQNRKWIYKNGHGDILK 420
Db 361 VLVVIVVCSIRKSSRTLKGKPRQDPSAIVEAGLKLKSMTQNRKWIYKNGHGDILK 420
Qy 361 VLVVIVVCSIRKSSRTLKGKPRQDPSAIVEAGLKLKSMTQNRKWIYKNGHGDILK 420
Db 361 VLVVIVVCSIRKSSRTLKGKPRQDPSAIVEAGLKLKSMTQNRKWIYKNGHGDILK 420
Qy 421 LVAQYQCSQWQDIYQFLCNASERVAFAFSNSYTAHERAYALQHNTIRGPEASLAQLIS 480
Db 421 LVAQYQCSQWQDIYQFLCNASERVAFAFSNSYTAHERAYALQHNTIRGPEASLAQLIS 480
Qy 421 LVAQYQCSQWQDIYQFLCNASERVAFAFSNSYTAHERAYALQHNTIRGPEASLAQLIS 480
Db 421 LVAQYQCSQWQDIYQFLCNASERVAFAFSNSYTAHERAYALQHNTIRGPEASLAQLIS 480
Qy 481 ALRQRHNDVYKEKIRGLMEDTQLETDKLALPMSPLSPSPLSPSPAKLENSALITVEP 540
Db 481 ALRQRHNDVYKEKIRGLMEDTQLETDKLALPMSPLSPSPLSPSPAKLENSALITVEP 540
Qy 541 SPQDKNKGFFYDESEPLRCDSTSSGSSALSRNGSFITKEKDTVLRQRVLDPCDQPIF 600
Db 541 SPQDKNKGFFYDESEPLRCDSTSSGSSALSRNGSFITKEKDTVLRQRVLDPCDQPIF 600
Qy 541 SPQDKNKGFFYDESEPLRCDSTSSGSSALSRNGSFITKEKDTVLRQRVLDPCDQPIF 600
Db 541 SPQDKNKGFFYDESEPLRCDSTSSGSSALSRNGSFITKEKDTVLRQRVLDPCDQPIF 600
Qy 601 DDMHLFLNPPEELRVTEBIPQAEDKLDRLFETIGVKSQEAQSTLLDSVSYSHLPDLL 655
Db 601 DDMHLFLNPPEELRVTEBIPQAEDKLDRLFETIGVKSQEAQSTLLDSVSYSHLPDLL 655
Qy 601 DDMHLFLNPPEELRVTEBIPQAEDKLDRLFETIGVKSQEAQSTLLDSVSYSHLPDLL 655
Db 601 DDMHLFLNPPEELRVTEBIPQAEDKLDRLFETIGVKSQEAQSTLLDSVSYSHLPDLL 655

RESULT 7
 US-09-042-785A-4
 ; Sequence 4, Application US/09042785A
 ; Patent No. 619151

GENERAL INFORMATION:
 ; APPLICANT: Busfield, Samantha J
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
 ; NUMBER OF INVENTION: 31
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/042,785A
 ; FILING DATE: 17-MAR-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/938,896
 ; FILING DATE: 26-SEP-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouas, Amy E
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: MEI-001CP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 253 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-09-042-785A-4

RESULT 8
 US-09-527-236A-19
 ; Sequence 19, Application US/09527236A
 ; Patent No. 635808

GENERAL INFORMATION:
 ; APPLICANT: Guo-Liang, Yu, Jian
 ; APPLICANT: Fan, Ping
 ; APPLICANT: Gantz, Reiner L.
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 ; FILE REFERENCE: PF315P1
 ; CURRENT APPLICATION NUMBER: US/09/527,236A
 ; CURRENT FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/1052,991
 ; PRIOR FILING DATE: 1997-06-11
 ; PRIOR APPLICATION NUMBER: 09/995,094
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/1226,019
 ; PRIOR FILING DATE: 1999-03-24
 ; PRIOR APPLICATION NUMBER: 60/134,220
 ; PRIOR FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 19
 ; LENGTH: 147
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-527-236A-19

Query Match 39.3%; Score 1359; DB 3; Length 253;
 Best Local Similarity 100.0%; Pred. No. 5.9e-113;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTPSSSTALACSRARRATAMIASLILLLIGLSTTAQEQKASNLTGTYHYDRA 60
 Db 1 MGTPSSSTALACSRARRATAMIASLILLLIGLSTTAQEQKASNLTGTYHYDRA 60

Qy 1 MGTPSSSTALACSRARRATAMIASLILLLIGLSTTAQEQKASNLTGTYHYDRA 60
 Db 1 MGTPSSSTALACSRARRATAMIASLILLLIGLSTTAQEQKASNLTGTYHYDRA 60

Qy 61 TQGVLTCDKCPAGTYVSEHCTNTSLRVCCSPVGFTRHENGIEKHDQSPCPWPMIEK 120
 Db 61 TQGVLTCDKCPAGTYVSEHCTNTSLRVCCSPVGFTRHENGIEKHDQSPCPWPMIEK 120

Qy 121 LPCALTDRECTCPGMFQSNATCAPIHVCYCPVGWGVRKKGTEEDVRCKQARGTFSDVP 180
 Db 121 LPCALTDRECTCPGMFQSNATCAPIHVCYCPVGWGVRKKGTEEDVRCKQARGTFSDVP 180

Qy 181 SSVMKCKAYTDCLSONLVLVTKPGETKEDNVCGTLPSPFSSSTSRSPGTAIFPRPEHMETHE 240
 Db 181 SSVMKCKAYTDCLSONLVLVTKPGETKEDNVCGTLPSPFSSSTSRSPGTAIFPRPEHMETHE 240

Db 241 VPSTTYVPK 249
 Qy 241 VPSTTYVPK 249

RESULT 9
 US-09-756-854-19

Sequence 19, Application US/097566854
 Patent No. 6667390
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 Fan, Ping
 GENTZ, Reiner
 TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: MD
 COUNTRY: US
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/756,854
 FILING DATE: 10-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/095,094
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoover, Kenley K.
 REGISTRATION NUMBER: 40,302
 REFERENCE/DOCKET NUMBER: PF375
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-8504
 TELEFAX: 301-309-8439
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 147 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-09-756-854-19

Query Match 24.3%; Score 841; DB 4; Length 147;
 Best Local Similarity 99.3%; Pred. No. 3.9e-67;
 Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 66 TCDKCPAGTYSEHCTNTSLRVCSSCPVGTTRHNGIEKHDQSPCPWPMIEK 125
 Db 1 TCDKCPAGTYSEHCTNTSLRVCSSCPVGTTRHNGIEKHDQSPCPWPMIEK 120

Qy 126 LTDRECTCPGMFQSNATCAPHTCPVQWGYTRKKGTETEDVRKOCARGTFSVPSSTMK 185
 Db 61 LTDRECTCPGMFQSNATCAPHTCPVQWGYTRKKGTETEDVRKOCARGTFSVPSSTMK 120

Query Match 24.3%; Score 841; DB 4; Length 147;
 Best Local Similarity 99.3%; Pred. No. 3.9e-67;
 Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 186 CKAYTDGLSQNLVVIKPGTETDNVCG 212
 Db 121 CKAYTDGLSQNLVVIKPGTETDNVCG 147

RESULT 10
 US-08-959-382-4
 Sequence 4, Application US/08959382

GENERAL INFORMATION:
 APPLICANT: DEEN, KEITH
 APPLICANT: HURLE, MARK
 APPLICANT: YOUNG, PETER
 APPLICANT: TAN, K. B.
 TITLE OF INVENTION: Tumor Necrosis Related Receptor, TR7

Sequence 4, Application US/09314844F
 Patent No. 666839
 GENERAL INFORMATION:
 APPLICANT: DEEN, KEITH CHARLES
 APPLICANT: HURLE, MARK R.
 APPLICANT: YOUNG, PETER
 APPLICANT: TAN, K. B.
 TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED

Current Application Number: US/09/314,844 F
 File Reference: GH-50017-1
 Title of Invention: DNA ENCODING TUMOR NECROSIS RELATED
 Patent No. 666839
 General Information:
 Prior Application Number: US 60/041,796
 Prior Filing Date: 1999-05-19
 Prior Application Number: US 60/041,796
 Prior Filing Date: 1997-04-02
 Prior Application Number: US 08/959,382
 Prior Filing Date: 1997-10-28
 Number of Seq ID Nos: 6

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 4
; LENGTH: 125
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-314-844F-4

Query Match 19.5%; Score 673; DB 4; Length 125;
 Best Local Similarity 100.0%; Pred. No. 2.9e-52;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSPSSSTALACCSRARRATATMAGSLLIGELSTTAPEQKASNLIGTYHVDRA 60
 Db 1 MGTSPSSSTALACCSRARRATATMAGSLLIGELSTTAPEQKASNLIGTYHVDRA 60

Qy 61 TGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFRHENGIEKHDSCOPCPNPIEK 120
 Db 61 TGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFRHENGIEKHDSCOPCPNPIEK 120

Qy 121 LPCAA 125
 Db 121 LPCAA 125

RESULT 12
; Sequence 6, Application US/09314844F
; Patent No. 6660839
; GENERAL INFORMATION:
; APPLICANT: HURLE, MARK R.
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K. B.
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED
; FILE REFERENCE: GH-50017-1
; CURRENT APPLICATION NUMBER: US/09/314.844F
; CURRENT FILING DATE: 1999-05-19
; PRIORITY NUMBER: US 60/041,796
; PRIORITY FILING DATE: 1997-04-02
; PRIORITY NUMBER: US 08/959,382
; PRIORITY FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 6
; LENGTH: 102
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-314-844F-6

Query Match 15.9%; Score 548; DB 4; Length 102;
 Best Local Similarity 97.0%; Pred. No. 2.9e-41;
 Matches 98; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 25 MTAGSLLIGELSTTAPEQKASNLIGTYHVDRA GTQVLTCDKCPAGTYVSEHCTNTS 84
 Db 1 MTAGSLLIGELSTTAPEQKASNLIGTYHVDRA GTQVLTCDKCPAGTYVSEHCTNTS 60

Qy 85 LRVCSSCPVGTFRHENGIEKHDSCOPCPNPIEKLPCAA 125
 Db 61 LRVCQQCPVGTFRHENGIEKHDSCOPCPNPIEKLPCAA 101

RESULT 13
; Sequence 30, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM: Floppy disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997

RESULT 14
; Sequence 31, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS: 31
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM: Floppy disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: MEI-001CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 84 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: internal
 US-09-042-785A-31

Query Match 12.5%; Score 431; DB 3; Length 84;
 Best Local Similarity 100.0%; Pred. No. 5.9e-31;
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 415 GIDILKVAAQGSQWQDIIYQLCNASEREVAAFSNGYTA
 Db 1 GIDILKVAAQGSQWQDIIYQLCNASEREVAAFSNGYTA
 Qy 475 LAQLISALQRHRRNDVYVKIRGLM 498
 Db 61 LAQLISALQRHRRNDVYVKIRGLM 84

RESULT 15
 US-09-227-236A-21
 Sequence 21, Application US/09527236A
 Patent No 6351508
 GENERAL INFORMATION
 APPLICANT: Ni, Jian
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Gantz, Reiner L.
 APPLICANT: Fan, Ping
 TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 FILE REFERENCE: P2375P1
 CURRENT APPLICATION NUMBER: US/09/527,236A
 CURRENT FILING DATE: 2000-03-16
 PRIOR APPLICATION NUMBER: 60/052,991
 PRIOR FILING DATE: 1997-06-11
 PRIOR APPLICATION NUMBER: 09/095,094
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/126,019
 PRIOR FILING DATE: 1999-03-24
 PRIOR APPLICATION NUMBER: 60/134,220
 PRIOR FILING DATE: 1999-05-14
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 21
 LENGTH: 67
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-527-236A-21

Query Match 10.2%; Score 352; DB 4; Length 67;
 Best Local Similarity 100.0%; Pred. No. 4.5e-24;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 429 QWQDIIYQLCNASEREVAAFSNGYTA
 Db 1 QWQDIIYQLCNASEREVAAFSNGYTA
 Qy 489 DVVEKIR 495
 Db 61 DVVEKIR 67

Scoring table:	BLOSUM62	Gapop:	10.0	Gapext:	0.5	ALIGNMENTS									
Searched:	141681 seqs, 5070155 residues	141681				RESULT ¹	TR21_HUMAN	STANDARD;	PRT;	655 AA.					
Total number of hits satisfying chosen parameters:						ID	O75509; Q96D66;								
Minimum DB seq length:	0					AC	O75509; Q96D66;								
Maximum DB seq length:	2000000000					DT	28-FEB-2003 (Rel. 41, Created)								
Post-processing:	Minimum Match 0%					DT	28-FEB-2003 (Rel. 41, Last sequence update)								
	Maximum Match 100%					DT	10-OCT-2003 (Rel. 42, Last annotation update)								
Database :	SwissProt 42.2*					DE	Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-related death receptor-6) (Death receptor 6).								
Scoring table:	BLOSUM62					GN	TNFRSF21 OR DR6.								
Perfect score:	3456					OS	Homo sapiens (Human)								
Sequence:	1 MGTPSPSSSTALACSRRIARR.....SQEASOTLILDSSVSHLPDLL 655					OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
						NCBI_TaxID	=9606;								
						OX									
						RN	[1]								
						RP	SEQUENCE FROM N.A.								
						RX	MEDLINE:98376343; PubMed=9714541;								
						RA	Pan G., Bauer J.H., Hazidas V.M., Wang S., Liu D., Yu G., Vincenz C., Agarwal B.B., Ni J., Dixit V.M.								
						RT	"Identification and functional characterization of DR6, a novel death domain-containing TNF receptor.";								
						RL	FEBS Lett. 431:351-356 (1998).								
						RN	[2]								
						RP	SEQUENCE FROM N.A.								
						RA	Parker A./								
						RL	Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.								
						RN	[3]								
						RP	SEQUENCE FROM N.A.								
						RC	TISSUE=brain and Colon;								
						RX	MEDLINE:22386257; PubMed=12477932;								
						RA	Klaussner R.D., Feingold E.A., Grouse L.H., Derge J.G., Schulter G.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,								
						RA	Alzquiero R.D., Zeeberg B.B., Buerger K.H., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tohjiyuki S., Carninci P., Prange C., Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Gibbs R.A., Villalobos F., Muzny D.M., Sodenberg E.J., Lu X., Gibbs R.A., Fately J., Heitton E., Kettman M., Madan A., Rodriguez S., Sauceda A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J.J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schenck A., Schein J.E., Jones S.J.M., Marrs M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";								
						RA	RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).							
						RL	-1- FUNCTION: May activate NF- κ B and JNK and promote apoptosis.								
						CC	-1- SUBUNIT: Associates with TRADD.								
						CC	-1- SUBUNIT/LOCATION: Type I membrane protein (Probable).								
						CC	-1- TISSUE/SPECIFICITY: Highly expressed in heart, brain, placenta, pancreas, lymph node, thymus and prostate. Detected at lower levels in lung, skeletal muscle, kidney, testis, uterus, small								
						CC	CC								

approximately 5-fold lower affinity for homotrimeric TNFSP1/lymphotoxin-alpha. The TRAF1/TRAFF2 complex recruits the apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2. The TNF receptor 2 mediates most of the metabolic effects of TNF-alpha.	261 CVMTQVKRKPLCQREAKVPHLEADKARG-----TOGPPEQQLLITAP 324
--!- SUBUNIT: Binds to TRAF2.	
--!- PTM: Phosphorylated, mainly on serine residues and with a very low level on threonine residues.	
--!- PTM: A soluble form (tumor necrosis factor binding protein 2) is produced from the membrane form by proteolytic processing.	
--!- CC-PROTEIN: Available under the name Enbrel (Immunex and Wyeth-Ayerst). Used to treat moderate to severe rheumatoid arthritis (RA). Enbrel consist of the extracellular ligand-binding portion of TNFR2 linked to an Immunoglobulin FC chain. It binds to TNF-alpha and blocks its interactions with receptors.	315 SMEATGGEKSSTPI-KGPKRGRHR 337 325 SSSSSLESSAASALDRRAPTRNQQ 349
--!- SIMILARITY: Contains 4 TNFR-Cys repeats.	
--!- DATABASE: NAME=PROW; NOTE=CD entry; CD120b entry; WWW=http://www.ncbi.nlm.nih.gov/prob/cd/cd120b.html; CC-PROTEIN: Enbrel; NOTE=CD entry on Enbrel; WWW="http://www.enbrel.com/".	
--!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel; CC-PROTEIN: Enbrel; NOTE=CD entry; CD120b entry; CC-PROTEIN: Enbrel; NOTE=CD entry on Enbrel; WWW="http://www.enbrel.com/".	
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--!- EMBL: M32315; AAA59929.1; -.	RESULT 4 T11B RAT STANDARD; PRT; 401 AA. ID T11B RAT AC 08777; DT 28-FEB-2003 (Rel. 41, Created) ID T11B RAT AC 08777; DT 28-FEB-2003 (Rel. 41, Last sequence update) ID T11B RAT AC 08777; DT 28-FEB-2003 (Rel. 41, Last annotation update) DE Tumor necrosis factor receptor superfamily member 11B precursor (Osteoprotegerin). DE TNFRSF1B OR OFG. OS Rattus norvegicus (Rat). OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116; RN [1] RP SEQUENCE FROM N.A. RC SOURCE=Embryonic intestine; RX MEDLINE=97262071; PubMed=9108485; RA Simonet W.S.; Lacey D.L.; Dunstan C.R.; Kelley M.; Chang M.-S.; Luetty R.; Nguyen H.Q.; Wooden S.; Bennett L.; Boone T.; Shimamoto G.; De Rose M.; Elliott R.; Colombero A.; Tan H.-L.; Trail G.; Sullivan J.; Davy E.; Bucay N.; Renshaw-Gegg L.; Hughes T.M.; Hill D.; Patterson W.; Campbell P.; Sander S.; Van G.; Tarpley J.; Derby P.; Lee R.; Suggs S.; Boyle W.J.; RT "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density."; RL Cell 89:309-319(1997). --!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis (By similarity). --!- SUBUNIT: Homodimer (By similarity). --!- SUBCELLULAR LOCATION: Secreted (By similarity). --!- INDUCTION: Upregulated by osteopontin. --!- SIMILARITY: Contains 4 TNFR-Cys repeats. --!- SIMILARITY: Contains 2 death domains.
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DR EMBL: U52532; AAC0622.1; JOINED. DR EMBL: U52533; AAC0622.1; JOINED. DR EMBL: U52534; AAC0622.1; JOINED. DR EMBL: U52535; AAC0622.1; JOINED. DR EMBL: U52536; AAC0622.1; JOINED. DR EMBL: U52537; AAC0622.1; JOINED. DR EMBL: U52538; AAC0622.1; JOINED. DR EMBL: U52539; AAC0622.1; JOINED. DR EMBL: U52540; AAC0622.1; JOINED. DR EMBL: U52541; AAC0622.1; JOINED. DR EMBL: U52542; AAC0622.1; JOINED. DR EMBL: U52543; AAC0622.1; JOINED. DR EMBL: U52544; AAC0622.1; JOINED. DR EMBL: U52545; AAC0622.1; JOINED. DR EMBL: U52546; AAC0622.1; JOINED. DR EMBL: U52547; AAC0622.1; JOINED. DR EMBL: U52548; AAC0622.1; JOINED. DR EMBL: U52549; AAC0622.1; JOINED. DR EMBL: U52550; AAC0622.1; JOINED. DR EMBL: U52551; AAC0622.1; JOINED. DR EMBL: U52552; AAC0622.1; JOINED. DR EMBL: U52553; AAC0622.1; JOINED. DR EMBL: U52554; AAC0622.1; JOINED. DR EMBL: U52555; AAC0622.1; JOINED. DR EMBL: U52556; AAC0622.1; JOINED. DR EMBL: U52557; AAC0622.1; JOINED. DR EMBL: U52558; AAC0622.1; JOINED. DR EMBL: U52559; AAC0622.1; JOINED. DR EMBL: U52560; AAC0622.1; JOINED. DR EMBL: U52561; AAC0622.1; JOINED. DR EMBL: U52562; AAC0622.1; JOINED. DR EMBL: U52563; AAC0622.1; JOINED. DR EMBL: U52564; AAC0622.1; JOINED. DR EMBL: U52565; AAC0622.1; JOINED. DR EMBL: U52566; AAC0622.1; JOINED. DR EMBL: U52567; AAC0622.1; JOINED. DR EMBL: U52568; AAC0622.1; JOINED. DR EMBL: U52569; AAC0622.1; JOINED. DR EMBL: U52570; AAC0622.1; JOINED. DR EMBL: U52571; AAC0622.1; JOINED. DR EMBL: U52572; AAC0622.1; JOINED. DR EMBL: U5

PT	DOMAIN	198	269	DEATH 1.	RN
PT	DOMAIN	270	365	DEATH 2.	RP
PT	SITE	400	400	INVOLVED IN DIMERIZATION (BY SIMILARITY).	SEQUENCE FROM N.A.
PT	DISULFID	41	54	BY SIMILARITY.	TISSUE-Lung cancer;
PT	DISULFID	44	62	BY SIMILARITY.	RC
PT	DISULFID	65	80	BY SIMILARITY.	RX
PT	DISULFID	83	97	BY SIMILARITY.	MEDLINE=98151033; PubMed=9492069;
PT	DISULFID	87	105	BY SIMILARITY.	RA
PT	DISULFID	107	118	BY SIMILARITY.	Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.,
PT	DISULFID	124	142	BY SIMILARITY.	RT
PT	DISULFID	145	160	BY SIMILARITY.	"Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits osteoclastogenesis in vitro."
PT	DISULFID	166	185	BY SIMILARITY.	RT
PT	CARBONYD	98	98	BY SIMILARITY.	RT
PT	CARBONYD	165	165	N-LINKED (GLCNAC. . .) (POTENTIAL).	RT
PT	CARBONYD	178	178	N-LINKED (GLCNAC. . .) (POTENTIAL).	RT
PT	CARBONYD	289	289	N-LINKED (GLCNAC. . .) (POTENTIAL).	RT
SQ	SEQUENCE	401 AA;	46192 MW;	FECEA31FD4E573A CRC64;	RT
Query Match	8.8%	Score 304.5;	DB 1;	Length 401;	RT
Best Local Similarity	28.6%	Pred. No. 7.8e-13;	Indels 41;	Gaps 9;	RT
Matches	91;	Conservative 44;	Mismatches 142;	Indels 41;	SEQUENCE FROM N.A., AND VARIANT ASN-3.
Qy	30	LLLGFLSTTAQ--PEQKASNLIGTYRHDRATGVLCDKPCAGTYVSEHCNTNSLEV 87	RC		
Db	10	LYPDLIIEWTQTBETPK-----YHYPETPQLLEDKCAAGTYKQHQHTVYRRTI 61	RX		
Qy	88	CCSSCPVGFTRHENGIEKHDGSDQGPFWPMIBKLPCAAALTDRECTCPGMFOSIATCAH 147	RA		
Db	62	CVPCPDYSYTDWSHTSDCVCSPVKELTQTVKQECNRINRVCECEGRYLELEFLCXH 121	RA		
Qy	148	TYCPVGNGVKGKGTEEDVRCQKARGTFSDVPSYMKCKAYTDQCLSONLUVTKPGTKT 207	RA		
Db	122	RSPPPGIGLQLGQTPEENNTVKRCRPGFSEBTSSKAPRCHTNGSSGLLIGKGNATH 181	RA		
Qy	208	DWVCGTLPSSSSTSSPGTAAFPREDEHMETHEPSSTTYPKGKN-----SPENSSSA 260	RA		
Db	182	DWVY----SGNREATONGIDVTLCEAFFFVPTK-TIPPNWLSVLDLSPGKVNAA 236	RA		
Qy	261	SYRPKVLSI1QEGTVP-----DNTSSAARKEDVINKTLPNQVNVHQGPQRHRI---- 309	RA		
Db	237	VERIKRPHSSQFQTFQLKLWKHON---RDOEMVTKKIQDIDCESSTYQRHIGHANLIT 292	RA		
Qy	310	--LKLPSMEEATGEEKS 325	RA		
Db	293	EQLRIL--MESLPGKTS 308	RA		
RESULT 5					
ID	T11B_HUMAN	STANDARD;	PRT;	401 AA.	
AC	Q003700_0602336; Q9UHP4;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	10-OCT-2003 (Rel. 42, Last sequence update)				
DE	Tumor necrosis factor receptor superfamily member 11B precursor				
DE	osteoprotegerin (osteoclastogenesis inhibitory factor).				
GN	TNFSF11B OR OPG OR OCIF.				
OS	Homo sapiens (Human)				
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
NCBI_TaxID=606;					
RN	SEQUENCE FROM N.A.				
RC	SEQUENCE-Kidney;				
RC	TISSUE-Kidney;				
RC	TISSUE-OPG;				
RC	TISSUE-OCIF.				
RA	Simone W.S., Lacey D.L., Dunsan C.R., Kelley M., Chang M.-S.,				
RA	Luetky R., Nguyen H.Q., Woodin S., Bennett L., Shimamoto G.,				
RA	Deroze M., Elliott R., Colombo A., Tan H.-L., Trail G., Sullivan W.,				
RA	Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D.,				
RA	Campbell P., Sander S., van G., Tarpley J., Derby P., Lee R.,				
RA	Suggs S., Boyle W.J.,				
RT	"Osteoprotegerin, a novel secreted protein involved in the regulation				
RT	of bone density."				

J. Biol. Chem. 273:14363-14367 (1998).	FT REPEAT 65	105	TNFR-CYS 2.
[9] CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.	FT REPEAT 107	142	TNFR-CYS 3.
RT MEDLINE-98144058; Pubmed=9418964;	FT REPEAT 145	185	TNFR-CYS 4.
RA Yamaguchi K.; Kinoshita M.; Goto M.; Kobayashi F.; Tsuda E.,	FT DOMAIN 198	269	DEATH 1.
RA Morinaga T.; Higashio K.	FT DOMAIN 270	365	DEATH 2.
RT "characterization of structural domains of human osteoclastogenesis.	FT SITE 400	400	INVOLVED IN DIMERIZATION.
RT inhibitory factor;"	FT DISULFID 41	54	BY SIMILARITY.
RT J. Biol. Chem. 273:5117-5123 (1998).	FT DISULFID 44	62	BY SIMILARITY.
RT J. Biol. Chem. 273:5117-5123 (1998).	FT DISULFID 65	80	BY SIMILARITY.
RT J. Biol. Chem. 273:5117-5123 (1998).	FT DISULFID 83	97	BY SIMILARITY.
RT J. Biol. Chem. 273:5117-5123 (1998).	FT DISULFID 87	105	BY SIMILARITY.
RT J. Biol. Chem. 273:5117-5123 (1998).	FT DISULFID 107	118	BY SIMILARITY.
RA MEDLINE=21395914; PubMed=11505389;	FT DISULFID 124	142	BY SIMILARITY.
RA Hofbauer L.C.; Neubauer A.; Heufelder A.E.;	FT DISULFID 145	160	BY SIMILARITY.
RT "Receptor activator of nuclear factor-kappaB ligand and	FT DISULFID 166	185	BY SIMILARITY.
osteoprotegerin: Potential implications for the pathogenesis and	FT CARBOHYD 99	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
treatment of malignant bone diseases.";	FT CARBOHYD 152	152	N-LINKED (GLCNAC. . .) (POTENTIAL).
CC RT FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes	FT CARBOHYD 165	165	N-LINKED (GLCNAC. . .) (POTENTIAL).
its function in osteoclastogenesis. Inhibits the activation of	FT CARBOHYD 178	178	N-LINKED (GLCNAC. . .) (POTENTIAL).
osteoclasts and promotes osteoclast apoptosis in vitro. Bone	FT CARBOHYD 289	289	N-LINKED (GLCNAC. . .) (POTENTIAL).
homostasis seems to depend on the local RANKL/OPG ratio. May also	FT VARIANT 3	3	K > N.
play a role in preventing arterial calcification. May act as decoy			/FTD=VAR 013439.
receptor for TRAIL and protect against apoptosis. TRAIL binding			C->S: ABOLISHES DIMERIZATION.
blocks the inhibition of osteoclastogenesis.			MISSING: ABOLISHES DIMERIZATION.
CC -1- SUBUNIT: Homodimer.	FT MUTAGEN 400	400	D -> A (IN REF. 1).
CC -1- SUBCELLULAR LOCATION: Secreted.	FT MUTAGEN 401	401	MISSING: ABOLISHES DIMERIZATION.
CC -1- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney, liver, spleen, thymus, prostate, ovary, small intestine, thymus, thyroid, lymph node, trachea, adrenal gland, testis, and bone marrow.	FT CONFLICT 263	263	EDF448867D86C71E CRC64;
CC Detected at very low levels in brain, placenta, and skeletal muscle. Highly expressed in fetal kidney, liver and lung.	FT CONFLICT 4 01 AA;	4 01 AA;	EDF448867D86C71E CRC64;
CC -1- INDUCTION: Upregulated by increasing calcium-concentration in the medium and estrogens. Downregulated by glucocorticoids.	FT SEQUENCE 8.7%; Score 301.5; DB 1;	Length 401;	Query Match
CC -1- PTM: N-Glycosylation. Contains sialic acid residues.	FT SEQUENCE Best Local Similarity 24.8%; Pred. No. 1, 2e-12;	1e-12;	Best Local Similarity
CC -1- SIMILARITY: Contains 4 TNFR-CYS repeats.	FT SEQUENCE Matches 102; Conservative 58; Mismatches 177; Indels 75; Gaps 13	1e-12;	Matches
CC -1- SIMILARITY: Contains 2 death domains.	FT SEQUENCE		1e-12;
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	Db 54 YRHVRDTRGQVLTCDKCPAGTYVSEHCTNTSLRVYCCSPVGTFRHENGIEKCHDCSOPC 111	111	YRHYDTRGQVLTCDKCPAGTYVSEHCTNTSLRVYCCSPVGTFRHENGIEKCHDCSOPC 111
CC -1- SIMILARITY: Contains 2 death domains.	Db 28 YLHYDEBTSHOLCDKCPGPTYLKOHCTARWKTVTCAPCDHYDTSWHTSDCELYCSPVC 87	87	YLHYDEBTSHOLCDKCPGPTYLKOHCTARWKTVTCAPCDHYDTSWHTSDCELYCSPVC 87
CC -1- SIMILARITY: Contains 4 TNFR-CYS repeats.	Qy 114 PWPMEKLP2PAAITDRECTPPGNEQSNTACPHPTVCPVGMGVKKGTETDVKCKQCAR 177	177	Qy 114 PWPMEKLP2PAAITDRECTPPGNEQSNTACPHPTVCPVGMGVKKGTETDVKCKQCAR 177
CC -1- SIMILARITY: Contains 2 death domains.	Db 88 KELQYVQECNRTHNRVCEKEKGRGLIEFCLKHSRSCPFGVYQAGTPERNITYKRCPD 141	141	Db 88 KELQYVQECNRTHNRVCEKEKGRGLIEFCLKHSRSCPFGVYQAGTPERNITYKRCPD 141
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	Qy 174 GTFSDPVSSYTKCKAYTDCLUSQNLVYVKGPTKEDTNVCCTLPLSSSTPSPGTAIFPRP 23 2	23 2	Qy 174 GTFSDPVSSYTKCKAYTDCLUSQNLVYVKGPTKEDTNVCCTLPLSSSTPSPGTAIFPRP 23 2
CC -1- SIMILARITY: Contains 2 death domains.	Db 148 GFPSNETSSK2PCKRHTNCVPGHLITQKGNTATHNIC---SONSESTOKG1DVTLC 203	203	Db 148 GFPGRHPRQNLHKHFDINEHLPWMTVFLLLVLLVIVVSSIRKSRTLKKGPQDPSAIV 38 3
CC -1- SIMILARITY: Contains 2 death domains.	Qy 234 EHMETHEVEPSSTYVPKGMN-----STESNSASSAVRPKVLSI1QEGTVP-----DNT 27 2	27 2	Qy 234 EHMETHEVEPSSTYVPKGMN-----STESNSASSAVRPKVLSI1QEGTVP-----DNT 27 2
CC -1- SIMILARITY: Contains 2 death domains.	Db 204 EAFFRAVPKTFPWNLSVLDVNLPGTKVNAESEVIRQHSSQEQTQOLLKWKHQN- 26 21	26 21	Db 204 EAFFRAVPKTFPWNLSVLDVNLPGTKVNAESEVIRQHSSQEQTQOLLKWKHQN- 26 21
DR EMBL: U94332; AAB3709.1;	Qy 280 SSARGKEDVNTKLPNLQVNVHQGPHHR-----ILKLPMSMEATGGFKSSTPK 32 9	32 9	Qy 280 SSARGKEDVNTKLPNLQVNVHQGPHHR-----ILKLPMSMEATGGFKSSTPK 32 9
DR EMBL: AB002116; BAA25910.1; -.	Db 262 --KQDQDIVKQIQQDLCNSVQRHIGANLTQEQLRIMESLPG-KRKGADIEKTIK 31 31	31	Db 262 --KQDQDIVKQIQQDLCNSVQRHIGANLTQEQLRIMESLPG-KRKGADIEKTIK 31 31
DR EMBL: AB008B22; BAA32076.1; -.	Qy 330 GPKRGHPRQNLHKHFDINEHLPWMTVFLLLVLLVIVVSSIRKSRTLKKGPQDPSAIV 38 3	38	Qy 330 GPKRGHPRQNLHKHFDINEHLPWMTVFLLLVLLVIVVSSIRKSRTLKKGPQDPSAIV 38 3
DR EMBL: AB008B21; BAA32076.1; -.	Db 318 ACK--PSDQIKLSSL-----WRI-----KNGDQTLKGML 34 4	34 4	Db 318 ACK--PSDQIKLSSL-----WRI-----KNGDQTLKGML 34 4
DR EMBL: BC030155; AAH30155.1; -.	Qy 390 EKAGIJKS-----MPTQNTREKNTIYVNCNGHGIIDL--KLVAAGVGSQWKDI 43 3	43 3	Qy 390 EKAGIJKS-----MPTQNTREKNTIYVNCNGHGIIDL--KLVAAGVGSQWKDI 43 3
DR EMBL: BC030155; AAH30155.1; -.	Db 347 H--ALKHSKTYHFPKPTVTQSLKTTTRFLHSFTMMKLYQKLFLMIGNQVOSV 3 9 6	3 9 6	Db 347 H--ALKHSKTYHFPKPTVTQSLKTTTRFLHSFTMMKLYQKLFLMIGNQVOSV 3 9 6
DR HSSP: P05942; 1 CDF.	RESULT 6		RESULT 6
DR Genew: HGNC:111909; TNFRSF1B.	T11B MOUSE		T11B MOUSE
DR MIM: 602643; -.	ID T11B MOUSE		ID T11B MOUSE
DR GO: GO:0005576; C:extracellular; TAS.	STANDARD;		STANDARD;
DR GO: GO:0005125; F:cytokine activity; TAS.	PRT: 401 AA.		PRT: 401 AA.
DR GO: GO:004872; receptor activity; TAS.			
DR GO: GO:0007165; P:signal transduction; TAS.			
DR GO: GO:0001501; P:skeletal development; TAS.			
DR InterPro: IPR00488; Deaf.			
DR Pfam: PF00020; TNFR_C6_3.			
DR SMART: SM00005; DEATH; 1.			
DR PROSITE: PS50017; DEATH DOMAIN; FALSE_NEG.			
DR PROSITE: PS50052; TNFR_NGFR_1; 1.			
DR PROSITE: PS50050; TNFR_NGFR_2; 2.			
DR Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.			
DR SIGNAL_1; 21 TUMOR NEFROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B.			
DR CHAIN_1; 22 TUMOR NEFROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B.			
FT PREPATRANT			
FT PREPATRANT			
OC Mammalia. Bivalvia: Bivalvia; Mollusca: Mollusca; Chordata: Chordata; Craniata: Craniata; Vertebrata: Vertebrata; Euteleostomi: Euteleostomi; OC Mammalia. Bivalvia: Bivalvia; Mollusca: Mollusca; Chordata: Chordata; Craniata: Craniata; Vertebrata: Vertebrata; Euteleostomi: Euteleostomi; OC Mammalia. Rodentia: Rodentia; Sciuromorpha: Sciuromorpha; Muridae: Muridae; Mus: Mus.			

RESULT	7
TR6B_HUMAN	STANDARD;
ID	PRT; 300 AA.
AC	095447;
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Tumor necrosis factor receptor superfamily member 6B precursor (Decoy receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M68).
DE	TNFRSF6B OR DCR3 OR TR6.
DE	GN
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_TaxID=9606;
CX	
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Fetal lung;
RX	Medline=9087326; PubMed=987321;
PTI	R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C., Dowd P., Huang A., Donanne C.J., Sherwood S.W., Baldwin D.J., Godowski P.J., Wood W.I., Gurin A.L., Hillian K.J., Cohen R.L., Godowski D., Botstein D., Ashkenazi A.; "Genomic amplification of a decoy receptor for Fas ligand in lung and colon cancer." Nature 395:699-703 (1998).
RN	[2]
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
RC	TISSUE=Prostate;
RX	Medline=9253915; PubMed=10318773;
PTI	R.W. Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.; "A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis." J. Biol. Chem. 274:13733-13736 (1999).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lung;
RX	Medline=21122600; PubMed=10655513;
PTI	Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V., Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.; "Overexpression of M6/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster." Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235 (2000).
RN	[4]
RP	SEQUENCE FROM N.A.
RA	Matthews L.;
RN	Submitted (NOV-2000) to the EMBL/GenBank/DDJB databases.
RN	[5]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lung, and Skin;
RX	Medline=21388257; PubMed=12477932;
RA	Strausberg R.L., Fengold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner J., Schuler G.D., Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong I., Stapleton M., Soares M.B., Balido M.P., Casavant T.L., Scheffler T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Prange C., Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEvian P.J., McKerian K.J., Malek J.A., Gunnarsson P.H., Richard S., Worley C.K., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalona D.K., Muzny D.M., Soedergran E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Lu J., Bouffard G.G., Blakesley R.W., Touchman J.W., Green D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rodriguez A.C., Bouffard G.G., Skalak M.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RA	Butfield T.S.N., Krzywinski M.J., Skalak R.M., Schnerr A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

and TNFSF6/FasL. Protects against apoptosis.																		
-!- SUBCELLULAR LOCATION: Secreted.																		
-!- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.																		
Detected in adult stomach, spinal cord, lymph node, trachea, spleen, colon and lung. Highly expressed in several primary tumors from colon, stomach, rectum, esophagus and in SW480 colon carcinoma cells.																		
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.																		
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<p>EMBL; AF104413; AAD03056_1; -.</p>																		
<p>EMBL; AF134240; AAD29688_1; -.</p>																		
<p>EMBL; AF217796; AAF35244_1; -.</p>																		
<p>EMBL; AF217793; AAF35285_1; -.</p>																		
<p>EMBL; AF217794; AAF35286_1; -.</p>																		
<p>EMBL; ALI12184; CAC03668_1; -.</p>																		
<p>EMBL; BC017065; AAH17065_1; -.</p>																		
<p>EMBL; BC034349; AAH34349_1; -.</p>																		
<p>HSSP; Q14763; 1D0G.</p>																		
<p>Genew; HGNC:11921; TNFRSF6B.</p>																		
<p>MIM; 603361; -.</p>																		
<p>GO; GO:0005625; C:soluble fraction; TAS.</p>																		
<p>GO; GO:0008189; F:apoptosis inhibitor activity; TAS.</p>																		
<p>GO; GO:0004877; F:receptor activity; TAS.</p>																		
<p>GO; GO:0006911; P:anti-apoptosis; TAS.</p>																		
<p>InterPro: IPR011368; TNFR_C6.</p>																		
<p>PFam: PF00020; TNFR_c6_4.</p>																		
<p>SMART: SM00208; TNFR_4.</p>																		
<p>PROSITE: PS00052; TNFR_NGFR_1.</p>																		
<p>PROSITE: PS50030; TNFR_NGFR_2.</p>																		
<p>Receptor; Apoptosis; Glycoprotein; Repeat; Signal.</p>																		
SIGNAL	1		29		TUMOR NECROSIS FACTOR RECEPTOR		SUPERFAMILY MEMBER 6B.											
	30		300		REPEAT		TNFR-CYS 1.											
	REPEAT		31		REPEAT		TNFR-CYS 2.											
	72		70		72		TNFR-CYS 3.											
	REPEAT		115		115		TNFR-CYS 4.											
	152		193		152		BY SIMILARITY.											
	DISUFID		49		62		BY SIMILARITY.											
	DISUFID		52		70		BY SIMILARITY.											
	DISUFID		73		88		BY SIMILARITY.											
	DISUFID		91		105		BY SIMILARITY.											
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RESULT 8		PROSITE; PSS0050; TNFR_NGFR_2; 3.	
TRIB_MOUSE	STANDARD;	PRT;	474 AA.
ID			
AC	P25119; P97893;		
DT	01-MAY-1992 (Rel. 22, Created) 01-MAY-1992 (Rel. 22, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Tumor necrosis factor receptor superfamily member 1B precursor (TUMOR necrosis factor receptor 2) (TNF-R2) (p75).		
DE	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX			
RN	[1] TaxID=100900;		
SEQUENCE FROM N.A.			
RRX	SEQUENCE FROM N.A. MEDLINE:91187885; PubMed=1849278;		
RA	Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,		
RA	Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,		
RA	Coleland N.G., Jenkins N.A., Smith C.A.;		
RT	"Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.";		
RT	Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).		
RR			
SEQUENCE FROM N.A.			
RRX	SEQUENCE FROM N.A.; PubMed=1645445;		
RA	Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,		
RA	Coleland N.G., Jenkins N.A., Smith C.A.;		
RT	"Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor";		
RT	Mol. Cell. Biol. 11:3020-3026 (1991).		
RR			
SEQUENCE OF 1-26 FROM N.A.			
RR	STRAIN=NOID;		
RA	Jacob C.O., Liu J.;		
RA	Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.		
RN			
RR	SEQUENCE OF 1-22 FROM N.A.		
RC	TISSUE=liver;		
RL	Kissoonchis M., Fellowes R., Feldmann M., Chernajovsky Y.;		
RL	Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: Receptor with high affinity for TNFRSF1/TNF-alpha and approximately 5-fold lower affinity for homotrimeric TNFRSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1/TNFR2 (By similarity).		
CC	-1- SUBUNIT: Binds to TRAF2 (By similarity).		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-1- SIMILARITY: Contains 4 TNF-Cys repeats.		
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CC	RESULT 9		
DR	TNRS_MOUSE	STANDARD;	PRT; 415 AA.
AC	P53284;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DR	10-OCT-2003 (Rel. 42, Last annotation update)		
DR	Tumor necrosis factor receptor superfamily member 3 precursor (Lympotoxin- <i>alpha</i> receptor).		
GN	LITER OR TNFRSF3 OR TNFR.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX			
RN	[1]_TaxID=10090;		
RC	SEQUENCE FROM N.A.		
DR	SPAIN-CVB; TISSUE=Lung;		
DR	MEDLINE=96072804; PubMed=7594541;		

RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A., Browning J.L., Ware C.P., "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding, and expression.", *J. Immunol.* 155:5280-5288 (1995).

[2] SEQUENCE FROM N.A. PubMed=8586432; MEDLINE=96163885;

RA Nakamura T., Tashiro K., Nakano M., Nakano T., Sasayama S., Honjo T., "The murine lymphotoxin-beta receptor cDNA: isolation by the signal sequence trap and chromosomal mapping.", *Genomics* 30:312-319 (1995).

[3] RN INTERACTION WITH TRAF5.
STRAIN=BALB/C;
RC MEDLINE=96278943; PubMed=86632399;

RA Nakano H., Oshina H., Chung W., Williams-Abbot L., Ware C.P., Yagita H., Okumura K., "TRAF5, an activator of NF-kappaB and putative signal transducer for the lymphotoxin-beta receptor.", *J. Biol. Chem.* 271:4661-4664 (1996).

CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing ILT4 and LTB₄ and for TNFSF4/LIGHT. Promotes apoptosis via TRAF3 and TRAF5. May play a role in the development of lymphoid organs (By similarity).

CC -!- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.

CC -!- Associates with TRAF3 and TRAF4 (By similarity).

CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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CC -!- DR U29173; ARAB68964_1; ARB008423; ARB00846; ARB00846_1; ARB00846_2; ARB00846_3; ARB00846_4; ARB00846_5; ARB00846_6; ARB00846_7; ARB00846_8; ARB00846_9; ARB00846_10; ARB00846_11; ARB00846_12; ARB00846_13; ARB00846_14; ARB00846_15; ARB00846_16; ARB00846_17; ARB00846_18; ARB00846_19; ARB00846_20; ARB00846_21; ARB00846_22; ARB00846_23; ARB00846_24; ARB00846_25; ARB00846_26; ARB00846_27; ARB00846_28; ARB00846_29; ARB00846_30; ARB00846_31; ARB00846_32; ARB00846_33; ARB00846_34; ARB00846_35; ARB00846_36; ARB00846_37; ARB00846_38; ARB00846_39; ARB00846_40; ARB00846_41; ARB00846_42; ARB00846_43; ARB00846_44; ARB00846_45; ARB00846_46; ARB00846_47; ARB00846_48; ARB00846_49; ARB00846_50; ARB00846_51; ARB00846_52; ARB00846_53; ARB00846_54; ARB00846_55; ARB00846_56; ARB00846_57; ARB00846_58; ARB00846_59; ARB00846_60; ARB00846_61; ARB00846_62; ARB00846_63; ARB00846_64; ARB00846_65; ARB00846_66; ARB00846_67; ARB00846_68; ARB00846_69; ARB00846_70; ARB00846_71; ARB00846_72; ARB00846_73; ARB00846_74; 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CC	- - PTM: Phosphorylated on serine residues.	Db	297 ----- SVDSOSLHDQDPNQSTQGPAPKGDSLYASLPPSKQEE----- 335
CC	- - SIMILARITY: Contains 4 TNFR-Cys repeats.	Qy	410 YCNHGHDILKLYAAQVGSQWQKDIYKFLCNASEREYAAFSNGY----- TADHERAYA 461
CC	- - SIMILARITY: Contains 1 death domain.	Db	336 ----- VKEULSSAETVRQL----- AGEIGYKEDLDFTRERSPARA 374
DR		Qy	462 ALQHWTIRGPESLAQLISARQHRNDVVEKI 494
DRSSP; E07174; INCR		Db	375 LLADWSAK-ETATLDALVALRKIQGDIABSL 406
InterPro: IPR00488; Death..			
PFam; PF00531; death_1..			
DR			
PFam; PF00220; TNFR_C6; 4.			
DR			
SMART; SMART0005; DEATH_1..			
DR			
SMART; SM00208; TNFR_3..			
DR			
PROSITE; PS00652; TNFR_NGFR_1..3..			
DR			
PROSITE; PS50050; TNFR_NGFR_2..3..			
DR			
PROSITE; PS50017; DEATH_DOMAIN_1..1..			
KW	Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;		
KW	Repeat; Phosphorylation; Signal;		
FT	SIGNAL 1 19 POTENTIAL.		
FT	CHAIN 20 416 TUMOR NECROSIS FACTOR RECEPTOR	RESULT 11	TNFR_HUMAN STANDARD PRT; 255 AA.
FT	DOMAIN 29 239 SUPERFAMILY MEMBER 16.	ID	TNFR_HUMAN
FT	TRANSPM 240 261 EXTRACELLULAR (POTENTIAL).	AC	007011;
FT	DOMAIN 262 416 POTENTIAL.	DT	01-FEB-1995 (Rel. 31, Created)
FT	REPEAT 23 57 CYTOPLASMIC (POTENTIAL).	DT	01-OCT-2003 (Rel. 42, Last sequence update)
FT	REPEAT 58 99 TNFR-CYS 1..	DE	Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen 11A)
FT	REPEAT 100 138 TNFR-CYS 2..	DE	(CD137 antigen).
FT	REPEAT 140 180 TNFR-CYS 3..	GN	TNFRSF9 OR ILA OR CD137.
FT	DOMAIN 333 410 DEATH..	OS	Homo sapiens (Human)
FT	DOMAIN 188 236 SER/THR-RICH.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Subteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
FT	DISULFID 24 35 BY SIMILARITY.	OC	
FT	DISULFID 36 49 BY SIMILARITY.	NCBI_TAXID=9606;	
FT	DISULFID 39 56 BY SIMILARITY.	RN	
FT	DISULFID 59 75 BY SIMILARITY.	RP	SEQUENCE FROM N.A.
FT	DISULFID 78 91 BY SIMILARITY.	RC	TISSUE-Blood;
FT	DISULFID 81 99 BY SIMILARITY.	RC	MEDLINE=9437434; PubMed=8088337;
FT	DISULFID 101 114 BY SIMILARITY.	RA	Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J., Schwarz H., Tuckwell J., Lotz M., Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G., "Molecular and biological characterization of human 4-1BB and its ligand.", Bur. J. Immunol. 24:2219-2227(1994).
FT	DISULFID 117 130 BY SIMILARITY.	RA	
FT	DISULFID 120 138 BY SIMILARITY.	RA	
FT	DISULFID 141 156 BY SIMILARITY.	RA	
FT	DISULFID 159 172 BY SIMILARITY.	RA	
FT	DISULFID 162 180 BY SIMILARITY.	RA	
FT	CONFICT 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).	RT	"A receptor induced by lymphocyte activation-factor/tumor-necrosis-factor receptor induced by nerve-growth-factor/tumor-necrosis-factor receptor of the human nerve-growth-factor/tumor-necrosis-factor family.", Gene 134:295-298(1993).
FT	CONFICT 36 36 C -> Y (IN REF. 2).	RT	
FT	CONFICT 173 173 T -> K (IN REF. 2).	RT	
FT	CONFICT 276 276 N -> S (IN REF. 2).	RT	
FT	CONFICT 396 396 K -> R (IN REF. 2).	RT	
SO	SEQUENCE 416 AA; 44654 MW; 6BCEAAB54F4D2D56 CRC64;	RN	REVISIION TO 107.
SO		RA	Schwarz H., Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
SO		RA	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
SO		RN	SEQUENCE FROM N.A.
SO		RC	TISSUE-Blood;
SO		RC	MEDLINE=94085799; PubMed=8262189;
SO		RA	Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E., Kwon B.S., "Characterization of human homologue of 4-1BB and its ligand.", Immunol. Lett. 45:67-73(1995).
SO		RA	SEQUENCE FROM N.A.
SO		RA	Pearce A., Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
SO		RN	SEQUENCE FROM N.A.
SO		RC	TISSUE-Kidney;
SO		RC	MEDLINE=22188257; PubMed=112477932;
Qy	67 CDKCPACTYSEHTCTNTSLRVCSSC-PVGFTRHENGIIKCHDQSQPWPMIEKLPCAA 125	RA	Strausberg R.L., Feingold E.A., Grouse L.H., Wagner L., Schuler G.D., Klausner R.D., Collins F.S., Buetow K.H., Schaefer C.F., Bhattacharyya S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.F., Jordan H., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Soares M.B., Bonaldo M.F., Cesavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland J., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., Mccowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Db	36 CRACNIGEYVQPC-GVNTQTCPELDSVTSATVCKPCTQ-CVGLHSNSAPCIV' 93	RA	
Qy	126 LTDRECTCPCGMFQS--NATGAPHTVCPCVGVRKGKTETEDVRCQKQARGTFSDFVSSV 183	RA	
Db	94 SDDAVCRCAAYSFQDELGSCKECSICEVFGMLFPCRSDQTYCEBCEGTFSDEANFV 153	RA	
Qy	184 MKCKAYTDCLSONLYVTKPTKETDNVCGTL-----PSFSSTSPPGTAFLPRESH 235	RA	
Db	154 DPCLPCTIC-BENENVKCETATDAECDLHPRWTTHPSLASSDSSPPITDPFNTEG 212	RA	
Qy	236 METHEVPSSTVPGKGNSTNSNSAS---VRPKVLSQEGTVPDNTSSARGKEDVNTK 291	RA	
Db	213 MATTLDIVITVGMSSQPVYSGRTADNLIVYCSLAAVUVGLVAYIAFKRWNNSCKQKQ 272	RA	
Qy	292 LFNLOVNVHQCGPHHRHIKLKLPNSNEATGEGKSSTPIKGPKRGHPRQNLKHFDINEHLP 351	RA	
Db	273 GANRPVNPQTSPS-----GEK-----LHSDSGQI----- 296	RA	
Qy	352 WMIVLFLVIVVYVCSIRKSSRTLKKGPQRDPSAIVK--AGLKKSMPTQNREKMY 409	RA	

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villanueva D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahney J., Helton M., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Madan A., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodiek A.C., Grinberg J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[7] INTERACTION WITH TRAF1; TRAF2 AND TRAF3.
MEDLINE=98078711; PubMed=9418902;
Arch R.H., Thompson C.B.; "4-1BB and OX40 are members of a tumor necrosis factor (TNF)-nerve growth factor receptor subfamily that bind TNF receptor-associated factors and activate nuclear factor kappaB.;" Mol. Cell. Biol. 18:558-565 (1998).

[8] IN
INTERACTION WITH TRAF1 AND TRAF2.
MEDLINE=98270914; PubMed=607025;
Saoulli K., Lee S.Y., Cammons J.L., Yeh W.C., Santana A., Goldstein M.D., Banga N., DeBenedete M.A., Mak T.W., Choi Y., Watts T.H.; "CD28-independent, TRAF2-dependent costimulation of resting T cells by 4-1BB ligand.;" J. Exp. Med. 187:1849-1862 (1998).

[9] IN
INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.
MEDLINE=21662677; PubMed=1803328;
Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.; "A novel leucine-rich repeat protein (LRR-1): potential involvement in 4-1BB-induced signal transduction.;" Mol. Cells 12:304-312 (2001).

-!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T cell activation.
-!- SUBUNIT: Interacts with TRAF1, TRAF2 AND TRAF3. Interacts with LRR-repeat protein 1/LRR-1.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
-!- DATABASE: NAME=PRO; NOTE=CD guide CDW137 entry; URL="http://www.ncbi.nlm.nih.gov/picow/cd/cdw137.htm".

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EMBL; U03391; AAA53133.1; -;
EMBL; L12954; AAA62498.1; -;
EMBL; AL009183; CAB57398.1; -;
EMBL; BC0005196; AAH0196.1; -;
PIR; I38426; I38426.
Genew; HGNC:111924; TNFRSF9.
MIM; 602250; -;
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005941; P:receptor activity; TAS.
GO; GO:0005917; P:induction of apoptosis; TAS.
InterPro; IPR013136; TNFRSF9.
Pfam; PF00020; TNFR_6'; 2.
SMART; SM00208; TNFR_2.
PROSITE; PS000652; TNFR_NGR_1'; 1.
PROSITE; PS550059; TNFR_NGR_2'; 1.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
SIGNAL; 1 17 POTENTIAL TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 9.
CHAIN 18 255

FT	DOMAIN	1.8	186	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	187	213	POTENTIAL.
FT	DOMAIN	214	255	CYTOPLASMIC (POTENTIAL).
FT	REPAT	1.7	45	TNFR-CYS 1.
FT	REPAT	4.7	86	TNFR-CYS 2.
FT	REPAT	8.7	118	TNFR-CYS 3.
FT	REPAT	11.9	159	TNFR-CYS 4.
FT	DOMAIN	214	255	INTERACTS WITH IRR-1.
FT	DISULFID	28	37	BY SIMILARITY.
FT	DISULFID	3.1	45	BY SIMILARITY.
FT	DISULFID	4.8	62	BY SIMILARITY.
FT	DISULFID	65	78	BY SIMILARITY.
FT	DISULFID	68	86	BY SIMILARITY.
FT	DISULFID	88	94	BY SIMILARITY.
FT	DISULFID	99	106	BY SIMILARITY.
FT	DISULFID	102	117	BY SIMILARITY.
FT	DISULFID	1.2	133	BY SIMILARITY.
FT	DISULFID	139	158	BY SIMILARITY.
FT	CARBHYD	13.8	138	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBHYD	14.9	149	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	255 AA;	27899 MW;	F3A563FE5EF0040 C064;
Query	Match	6.8%	Score 235.5 , DB 1;	Length 255;
Query	Best Local Similarity	30.4%	Pred. No. 1.4e-08;	
Query	Matches 63; Conservative	24;	Mismatches 77; Indels 43; Gaps 8;	
Query	25 MIAGSSLLLGFLSTTAQPEQKASNLLGTYRHVRDRA	70	CTPKAGTVSEHNTNS 84	
Db	8 IVATLVLVINFERTSLQD-----	70	PCSNCPAGTF-----	CDNNR 41
Query	85 LVRVSCPVGTVPHENIJEKCHDCSOCPWNMIEKLPCAAATDRE	70	CTPKGMFQONATC 144	
Db	42 NQIISCPCPNSFS-SAGGQRTCDICRQ-CKGYFRTRKECSSTNSAEDCTGPHCJGAGC 99	70	99	
Query	145 AP-HTVCVPGVYRKKGTEEDVYRCKOCARGTFSVDYPSVNVKCKAYTDCLUSQNLVYTKPG 203	70	203	
Db	100 SMKEQDCQGQELTRKG-----CRQCCFGTFNDQDERRGI--CRPTWNCSDGKSVLVNG 150	70	150	
Query	204 TKETDNVCGTLP-----FSSSTSPPSP 225	70		
Db	151 TKERDVVCCPSPADLSPGASSVTPPEAP 177	70		
RESULT 12				
TNRS5_MOUSE				
AC	ID	TNR5_MOUSE	STANDARD;	
AC	P27112	Q99NE0; Q99NE2; Q99NE3;	PRT;	289 AA.
DT	01-AUG-1992	(Rel. 23, Created)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)		
DT	10-DEC-2003	(Rel. 42, Last annotation update)		
DE	Tumor necrosis factor receptor superfamily member 5 precursor			
DE	(CD40L receptor) (B-cell surface antigen CD40) (BB50) (CDw40).			
GN	TNFSF5 OR CD40.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Butheria; Rodentia; Sciurognathi; Murinae; Mus.			
RN	[1] _TAXID=10090;			
RP	SEQUENCE FROM N.A. (ISOFORM I).			
RX	MEDLINE=92105763; Published=1370315;			
RA	Torres R.M.; Clark E.A.;			
RA	"Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation."			
RL	J. Immunol. 148:620-626(1992).			
RN	[2]			
RP	STRAIN=BALB/c;			
RA	Torres R.M.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM I).			
RC	STRAIN=BALB/c; TISSUE=Liver;			
RC	MEDLINE=3305186; Published=1281194;			

Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A., Howard M., Cockayne D.A.; "Genomic structure and chromosomal mapping of the murine CD40 gene." ; *J. Immunol.* 149:3921-3926(1992).

[4] SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS II, III, IV AND V). MEDLINE=2117110; PubMed=11172023; MEDLINE=91184010; PubMed=7533327; MEDLINE=93182184; PubMed=8790348; MEDLINE=93182184; PubMed=8790348; Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.; "Regulation of CD40 function by its isoforms generated through alternative splicing." ; *Proc. Natl. Acad. Sci. U.S.A.* 98:1751-1756 (2001).

[5] INTERACTION WITH TRAF3. MEDLINE=91184010; PubMed=11172023; Cheng G., Cleary A.M., Ye Z.-S., Hong D.J., Lederman S., Baltimore D.; Ishida T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Watanne T., Yamamoto T., Inoue J.-I.; "TRAF5, a novel tumor necrosis factor receptor-associated factor family protein, mediates CD40 signaling"; *Proc. Natl. Acad. Sci. U.S.A.* 93:9437-9442 (1996).

-!- FUNCTION: Receptor for TNFSF5/CD40L

-!- SUBUNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1, TRAF2, and TRAF6 (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV and V); secreted (isoform II).

-!- ALTERNATIVE PRODUCTS

Event=Alternative splicing; Named isoforms=5;

Name=I;

IsodID=P27512-1; Sequence=Displayed;

Name=II;

IsodID=P27512-2; Sequence=VSP_006444; VSP_006447;

Name=III;

IsodID=P27512-3; Sequence=VSP_006477; VSP_006478;

Name=IV;

IsodID=P27512-4; Sequence=VSP_006479; VSP_006480;

Name=V;

IsodID=P27512-5; Sequence=VSP_006476;

-!- SIMILARITY: Contains 4 TNFR-Cys repeats.

[6] INTERACTION WITH TRAF5. MEDLINE=93182184; PubMed=8790348; Ishida T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Watanne T., Yamamoto T., Inoue J.-I.; "TRAF5, a novel tumor necrosis factor receptor-associated factor family protein, mediates CD40 signaling"; *Proc. Natl. Acad. Sci. U.S.A.* 93:9437-9442 (1996).

-!- FUNCTION: Receptor for TNFSF5/CD40L

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-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV and V); secreted (isoform II).

-!- ALTERNATIVE PRODUCTS

Event=Alternative splicing; Named isoforms=5;

Name=I;

IsodID=P27512-1; Sequence=Displayed;

Name=II;

IsodID=P27512-2; Sequence=VSP_006444; VSP_006447;

Name=III;

IsodID=P27512-3; Sequence=VSP_006477; VSP_006478;

Name=IV;

IsodID=P27512-4; Sequence=VSP_006479; VSP_006480;

Name=V;

IsodID=P27512-5; Sequence=VSP_006476;

-!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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EMBL; M83112; AAB08105; 1; -.

EMBL; M84126; AAA37404; 1; -.

EMBL; M94129; AAA37404; 1; JOINED.

EMBL; M94128; AAA37404; 1; JOINED.

EMBL; M94127; AAA37404; 1; JOINED.

EMBL; A041387; CAC29427; 1; -.

EMBL; A041388; CAC29428; 1; -.

EMBL; A041389; CAC29429; 1; -.

EMBL; A041390; CAC29430; 1; -.

PIR; A46476; A46479.

DDR; HSSP; P22942; 1CDF.

MGD; MGI_883336; TNFRSF5.

InterPro; IPR008063; Fas receptor.

InterPro; IPR001368; TNFRSF5.

PRINTS; PRO1680; FASRECEPTOR.

PRINTS; PRO020208; TNFR; 4.

PROSITE; PS00652; TNFR_NGFR_1; 1.

PROSITE; PS50050; TNFR_NGFR_2; 4.

Receptor; PMS5005; TNFR_NGFR_2; 4.

kw

RESULT 13	TNR3	HUMAN	STANDARD;	FRT;	435 AA.
ID	TNR3_HUMAN				
AC	P36541;				
DT	01-OCT-1994	(Rel. 29, Created)			
DT	01-OCT-1994	(Rel. 29, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 3 precursor				
DE	(Lyphotrophin-beta receptor) (Tumor necrosis factor receptor 2 related protein)				
DE	(Tumor necrosis factor C receptor).				
GN	LTBR OR TNFRSF3 OR TNFCR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OC					
OX					
OX					
OX					
					[1]
					NCBI_TaxID=9606;
					RN

Db	164	NNHCVPCCKACHFQNTSSPSSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLEPLPENSG	223
Qy	221	T 221	
Db	224	T 224	
RESULT 14			
RETRN5_BOVIN	STANDARD;	PRT;	269 AA.
ID ID_	TNR5_BOVIN		
Q28703 ;			
DT DT_	01-NOV-1997 (Rel. 35, Created)		
DT DT_	01-NOV-1997 (Rel. 35, Last sequence update)		
DT DT_	10-OCT-2003 (Rel. 42, Last annotation update)		
DE DE_	Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (Fragment).		
OS OS_	Bos taurus (Bovine).		
OC OC_	Eukaryote; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Bovidae; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.		
NCBI_TaxID=9913;			
RN RN_			
RP RP_			
SEQUENCE FROM N.A.			
MEDLINE=7281252 ; PubMed=9155560;			
RX RX_			
Hirano A., Brown W.C., Estes D.M.;			
"Cloning, expression and biological function of the bovine CD40 homologue: role in B-lymphocyte growth and differentiation in cattle.",			
Immunity 90:294-300(1997).			
CC CC_	FUNCTION: Receptor for TNFSF5/CD40L.		
CC CC_	SUBUNIT: Interacts with TRAF1, TRAF2, TRAF5 and TRAF6 (By similarity).		
CC CC_	SUBCELLULAR LOCATION: Type I membrane protein.		
CC CC_	SIMILARITY: Contains 4 TNFR-Cys repeats.		
CC CC_			
CC CC_	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC CC_			
EMBL; US7745; AAC88710_1; -			
DR DR_			
HSSP; P25942; ICDP; InterPro; IPR008033; Fas receptor.			
DR DR_			
InterPro; IPR001368; TNFR_c6.			
PRINTS; PRO00020; TNFR_c6_4.			
DR DR_			
SMART; SMO0208; TNFR_c4.			
DR DR_			
PROSITE; PS000652; TNFR_NGFR_1; 1.			
DR DR_			
PROSITE; PS50050; TNFR_NGFR_2; 1.			
CC CC_			
REceptor; Transmembrane; Glycoprotein; Repeat; Signal.			
CC CC_			
SIGNAL_1 19			
CHAIN_20 19			
FET_20 >269			
FET_20 TUNER_NECROSIS_FACTOR_RECECTOR			
FET_20 SUPERFAMILY_MEMBER_5.			
FET_20 EXTRACELLULAR_(POTENTIAL).			
FET_20 POTENTIAL.			
FET_20 CYTOPLASMIC_(POTENTIAL).			
FET_20 TUNER-CYS_1.			
FET_20 TUNER-CYS_2.			
FET_20 TUNER-CYS_3.			
FET_20 TUNER-CYS_4.			
FET_20 DISULFID_26 37			
FET_20 DISULFID_26 38			
FET_20 DISULFID_26 51			
FET_20 DISULFID_26 59			
FET_20 DISULFID_60 77			
FET_20 DISULFID_61 103			
FET_20 DISULFID_104 144			
FET_20 DISULFID_145 187			
FET_20 DISULFID_216 193			
FET_20 DOMAIN_194 215			
FET_20 DOMAIN_216 >269			
FET_20 DOMAIN_25 60			
FET_20 DOMAIN_60 59			
FET_20 DOMAIN_61 59			
FET_20 DOMAIN_62 77			
FET_20 DOMAIN_83 103			
FET_20 DOMAIN_105 119			
FET_20 DOMAIN_111 116			
FET_20 DOMAIN_125 143			
FET_20 DOMAIN_153 153			
FET_20 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FET_20			
FT FT_	CARBHYD 180		
FT FT_	NON_TER 269		
SQ SQ_	29933 MW;		
SQ SQ_	746903F30F95F387 CRC64;		
SQ SQ_			
Query Match 6.6%; Score 227; DB 1; Length 269;			
Best Local Similarity 33.7%; Pred. No. 5; 6e-08;			
Matches 55; Conservative 17; Mismatches 65; Indels 26; Gaps 4;			
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Db Db_	36 LCCDLPPGQKLVNDCTEVSKTEQSCGKGEEFLSTNREKYCHEHRYCN-----84		
QY QY_	122 PCAL-----TDRBCTCPGMQSNAT---CAHTVCPVGMGTRKGKGTETDVRC 169		
Db Db_	85 PNGLRRIQSEGTNTDTCVYBQGQHCTSHTECSTPHSLCLPGFQVQIATGLLDTVC 144		
QY QY_	170 QCARGTFSDVPSVMMKRAYTDLSQNLVVRPGTKETDVNCG 212		
Db Db_	145 PCPLGFSSNVSSAFKCHRWTISCCRKGVLVEQHVGTKNDVVCG 187		
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ID ID_VT2_MIXXVL			
RN RN_VT2_MIXXVL			
PRT PRT_VT2_MIXXVL			
STANDARD STANDARD_VT2_MIXXVL			
PRT PRT_VT2_MIXXVL			
AC AC_P29625;			
DT DT_01-APR-1993 (Rel. 25, Created)			
DT DT_01-APR-1993 (Rel. 25, Last sequence update)			
DE DE_Tumor necrosis factor soluble receptor precursor (Protein T2).			
GN GN_M002L OR T2.			
RN RNSEQUENCE FROM N.A.			
RN RN_VT2_MIXXVL			
RN RN_P29625;			
RN RN_Upton C., Macen J.L., Schreiber M., McFadden G.;			
RN RN_Myxoma virus expresses a secreted protein with homology to the tumor virus.			
RN RN_leporipoxvirus.			
RN RN_TaxID=31530;			
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RN RN_RX			
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RN RN_Upton C., Macen J.L., Schreiber M., McFadden G.;			
RN RN_Myxoma virus expresses a secreted protein with homology to the tumor virus.			
RN RN_virology 194:370-382(1991).			
RN RNSEQUENCE FROM N.A.			
RN RN_RX			
RN RN_MEDLINE=20032073; PubMed=10562494;			
RN RN_Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,			
RN RN_RA_Macallay C., Willer D., Evans D., McFadden G.;			
RN RN_RT_The complete DNA sequence of myxoma virus.;			
RN RN_Virology 264:295-318(1999).			
CC CC_- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL.			
CC CC_- ANTI-VIRAL EFFECTS: THE CYTOKINE.			
CC CC_- SIMILARITY: Contains 4 TNFR-Cys repeats.			
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CC CC_Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,			
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CC CC_RT_RT_Myxoma virus expresses a secreted protein with homology to the tumor virus.			

RW Receptor; Glycoprotein; Repeat; Signal. POTENTIAL.
 FT SIGNAL 1 16 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
 FT CHAIN 17 326 TNFR-CS 1.
 FT REPEAT 27 62 TNFR-CS 2.
 FT REPEAT 63 104 TNFR-CS 3.
 FT REPEAT 105 147 TNFR-CS 4.
 FT REPEAT 148 186 TNFR-CS 4.
 FT DISULFID 28 39 BY SIMILARITY.
 FT DISULFID 40 53 BY SIMILARITY.
 FT DISULFID 43 61 BY SIMILARITY.
 FT DISULFID 64 79 BY SIMILARITY.
 FT DISULFID 82 96 BY SIMILARITY.
 FT DISULFID 86 104 BY SIMILARITY.
 FT DISULFID 106 120 BY SIMILARITY.
 FT DISULFID 123 146 BY SIMILARITY.
 FT DISULFID 129 149 BY SIMILARITY.
 FT DISULFID 164 165 BY SIMILARITY.
 FT CARBOYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 326 AA: 35208 MW: ABBF027E947292FF CRC64;

Query Match 6.3%; Score 218.5; DB 1; Length 326;
 Best Local Similarity 36.8%; Pred. No. 2.6e-77;
 Matches 50; Conservative 10; Mismatches 69; Indels 7; Gaps 2;

Qy 65 LTCDKCPAGTYSEHCMNTSLRVCSSPGFTRIENGIEKCHDSDSQPCWPMLIEKLPCA 124
 Db 38 LCCTSCPGSIASRLCCPGSDTVCSPKNEFTASTNHAACVSCRGCTGHLSSEQSCD 97

Qy 125 ALTDRECTCPPEMF-----QSNATCPFHITCPVGNIGVRKKGTTETEDVRLRKQCARGTFS 178
 Db 98 KTRDRVDCSAGNYCLIKGQEGCRICAPKTKPAGIGV-SGHTRIGDVLCTKPRTYSD 156

Qy 179 VPSSVMKCKAYTDCLS 194
 Db 157 AVSSTERCTSSPNYIS 172

Search completed: September 21, 2004, 22:41:45
 Job time : 27 secs



GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: September 21, 2004, 22:35:52 ; Search time 130 Seconds

(without alignments)

1589.726 Million cell updates/sec

Q80500 gallus gallus gall

Q7YR15 canis familiaris

Q8UY53 vaccinia virus

Q72762 cowpox virus

Q9DJ12 cowpox virus

Q7T2H3 oncornynchus

Q57117 cowpox virus

Q57118 cowpox virus

Q57121 cowpox virus

Q57119 cowpox virus

Q7ZZY4 gallus gallus gall

Q8WMPQ2 ovis musculus

Q8K2X6 mus musculus

Q57100 monkeypox virus

Q57105 monkeypox virus

Q57291 monkeypox virus

Q8SG34 sus scrofa

Q8JFV6 brachydano

Q57099 monkeypox virus

Q85308 cowpox virus

Q57115 cowpox virus

Q57101 monkeypox virus

Q57277 monkeypox virus

Q57103 monkeypox virus

Q57102 monkeypox virus

Q57116 cowpox virus

Q57305 cowpox virus

Q57120 cowpox virus

Q57122 cowpox virus

US-10-663-157-2

Perfect score: 3456

Sequence: 1 MGTPSSSTALASCRIARR.....SQEASQTILDSSVYSHLPDLL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_ivirus:*

16: sp_bacteriophage:*

17: sp_archaea:*

17 257 7.4 462 13 Q80500 gallus gallus gall

18 250 7.2 274 6 Q7YR15 canis familiaris

19 248.5 7.2 167 12 Q8UY53 vaccinia virus

20 248.5 7.2 167 12 Q72762 cowpox virus

21 240.5 7.0 167 12 Q9DJ12 cowpox virus

22 240.5 7.0 167 12 Q7T2H3 oncornynchus

23 238 6.9 351 12 Q57117 cowpox virus

24 237.5 6.9 360 12 Q57118 cowpox virus

25 233 6.7 351 12 Q57121 cowpox virus

26 232.5 6.7 347 12 Q57119 cowpox virus

27 231 6.7 146 13 Q7ZZY4 gallus gallus gall

28 231 6.7 6 146 13 Q7ZZY4 gallus gallus gall

29 231 6.7 289 11 Q8R2X6 mus musculus

30 230.5 6.7 349 12 Q57100 monkeypox virus

31 230 6.7 348 12 Q57108 monkeypox virus

32 230 6.7 348 12 Q57277 monkeypox virus

33 230 6.7 348 12 Q57103 monkeypox virus

34 228.5 6.6 349 12 Q57102 monkeypox virus

35 228 6.6 347 12 Q57115 cowpox virus

36 227.5 6.6 349 12 Q57101 monkeypox virus

37 227.5 6.6 349 12 Q57291 monkeypox virus

38 227 6.6 278 6 Q8BSQ34 sus scrofa

39 226 6.5 317 13 Q8JFV6 brachydano

40 225.5 6.5 349 12 Q57099 monkeypox virus

41 225 6.5 355 12 Q85308 cowpox virus

42 223.5 6.5 350 12 Q57116 cowpox virus

43 221.5 6.4 349 12 Q57305 cowpox virus

44 216.5 6.3 326 12 Q57120 cowpox virus

45 214.5 6.2 326 12 Q57122 cowpox virus

ALIGNMENTS

RESULT 1

Q8BZU6

PRELIMINARY;

PRT: 573 AA.

ID Q8BZU6

AC Q8BZU6;

DT 01-MAR-2003 (TREMBLrel). 23, (Created)

DT 01-MAR-2003 (TREMBLrel). 23, (Last sequence update)

DT 01-OCT-2003 (TREMBLrel). 25, (Last annotation update)

DE Death receptor 6.

GN TNFRSF21 OR AA959878.

OS Mus musculus (Mouse)

OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.

OX NCBI_TaxID:10990;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Colon;

RX MEDLINE=2354683; PubMed=12466851;

RA The FANTOM Consortium,

the RIKEN Genome Exploration Research Group, Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60770 full-length cDNAs.";

RL Nature 420:533-573 (2002).

DR MGI:2154075; InfraT21.

DR GO:GO:0004822; Fc receptor activity; IFA.

DR MGI:AK033529; BAC28342.1.

DR InterPro; IPR00488; Death.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00531; death_1.

DR Pfam; PF0020; TNFR_C6_3.

DR SMART; SM00005; DEATH_1.

DR SM00208; TNFR_3.

DR PSS0017; DEATH_DOMAIN_1.

DR PROSITE; PS50052; TNFR_NGFR_1.

DR PROSITE; PS50050; TNFR_NGFR_2.

DR PROSITE; PS50056; TNFR_NGFR_3.

DR SEQUENCE 573 AA; 63506 MW;

DR BC883B4EC8F2FE94 CRC64;

DR BC883B4EC8F2FE94 CRC64;

DR BC883B4EC8F2FE94 CRC64;

Query Match 8 Score 2715; DB 11; Length 573;

Best Local Similarity 89.9%; Pred. No. 1.4e-218;

Best Local Similarity 89.9%; Pred. No. 1.4e-218;

SUMMARIES

*

Result No. Score Query Match Length DB ID Description

1 2715 78.6 573 11 Q8BZU6

2 2356 68.2 651 13 Q9BSM6

3 453 13.1 132 13 Q9Y18

4 354 10.2 83 13 Q8UW0

5 326.5 9.4 457 4 Q8VVS6

6 308 8.9 285 13 Q90W71

7 307 8.9 285 13 Q90YS6

8 281.5 8.1 474 11 Q80WY6

9 278 8.0 186 13 Q7ZZY5

10 275.5 8.0 433 11 Q91ZM6

11 275.5 8.0 459 11 Q62327

12 275.5 7.8 302 13 Q9PUS0

13 268.5 7.6 482 11 Q88734

14 262.5 7.6 467 13 Q800IO

15 262 7.6 275 11 Q80WM9

16 259.5 7.5 11 Q80500

SEQUENCE FROM N.A.							
B	Brigham J.T.	Bobe J.	Goetz F.W.	Johnson A.L.			
A	"Conservation of Death Receptor-6 (DR6) in avian and piscine vertebrates",						
A	Biochem. Biophys. Res. Commun. 0:0-0(2001).						
A	EMBL: AF302492; AAL009310; 1.						
R	GO: 0004872; F: receptor activity; IEA.						
R	InterPro: IPR011368; INPR-C6.						
R	Pfam: PF00020; TNFR_C6; 2.						
R	SMART: SM00208; TNFR; 2.						
R	PROSITE: PS00652; TNFR_NGFR_1; 1.						
R	PROSITE: PS50050; TNFR_NGFR_2; 1.						
W	Receptor.						
W	NON_TER	1					
W	NON_TER	132	132	MW;	B01FED44260C1EB5	CRC64;	
Q	SEQUENCE	AA;	14303				
Q	Query Match		13.1%	Score 453;	DB 13;	Length 132;	
Q	Best Local Similarity		56.1%	Pred. No. 5.2e-30;			
Q	Matches 74;	Conservative	25;	Mismatches 33;	Indels 0;	Gaps 0;	
Y	74	TYVSEIICNTSLRVCGSCPVGTFHENGEBRKHCSQPCPWMTKLKPAAALDRECTC	133				
b	1	TFVSRHCTQINVRDSCRCDBGTFTENGHQCHCRRCRPRAPLVEKVPTATSDRRICT	60				
Y	134	PPGMFOSNATCAPHITYCPVWKGVRKGTEPDVRCQCARFTFSQDVPSSYMKCKAYTDC1	193				
b	61	PPDTFTQGDSTAHSLCPVGSVKKRGNDVEDVRCKAARGFSFSDMASSVLRCKHTDC1	120				
Y	194	SQNLVVIKPGTK 205					
b	121	AQSPLPLAAG 132					

RESULT 4							
BUNJ0	OBUNJ0	PRELIMINARY;	PRT;	83	AA.		
D	QBUUNJ0;						
C	QBUUNJ0;	01-MAR-2002	(TREMBLrel.	20,	Created)		
T	01-MAR-2002	(TREMBLrel.	20,	Last sequence update)			
T	01-JUN-2003	(TREMBLrel.	24,	Last annotation update)			
E	Death receptor	(Fragment).					
S	Galus gallus (Chicken)						
C	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallinae.						
C	NCBI_TaxID=9031;						
X	[1]						
N		SEQUENCE FROM N.A.					
P		SEQUENCE FROM N.A.					
C		TISSUE=Ovary;					
A		Shi Z, Onagbesan O.M., Williams J. /					
A		"Apoptosis in chicken ovary.";					
T		Submitted (Oct-2001) to the BMBL/GenBank/DBJU databases.					
T		EMBL: AF325122; AA135560.1; -.					
R		GO: 0004872; P: receptor activity; IEA.					
R		GO: 0007165; P: receptor transduction; IEA.					
R		InterPro: IPR000488; Death.					
R		Pfam: PF00531; dearth; 1.					
R		PROSITE; PS50017; DEATH_DOMAIN; 1.					
R		Receptor.					
W		NON_TER	1				
W		NON_TER	83	83			
W		SEQUENCE	83	AA;	9506 MW;	28F8C880F655FADC CRC64;	
Y		Query Match	10.2%		Score 354;	DB 13;	Length 83;
Y		Best Local Similarity	94.4%		Pred. No. 5.2e-22;		
Y		Matches	68;	Conservative	2;	Mismatches	0;
Y						Indels	Gaps
b		434 YQFLCNASEREEVAFAFNSNGYADHERAYAAQHWTIRGPEASLAQIISALRQHRRNDVVK	493				0;
b		1 YQFLCNASEREEVAFAFNSNGYADHERAYAAQHWTIRGPEASLAQIISALRQHRRNDVVK	60				
Y		494 IRGLMDTQLE	505				

Db	RESULT 5	PRELIMINARY;	PRT;	457 AA.
	Q8TVS6	PRELIMINARY;	PRT;	457 AA.
AC	Q8TVS6;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Similar to tumor necrosis factor receptor superfamily, member 1B (Fragment).			
DE	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Muscle;			
RA	Strausberg R.			
RL	Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL: BCO42167; AAH42167.1; -			
DR	GO: GO:004872; Fix receptor activity; IFA.			
DR	IntPro; IPR01368; TNFR_c6.			
DR	Pfam; PF00020; TNFR_c6; 4.			
DR	SMART; SM00208; TNFR_3.			
DR	PROSITE; PS00052; TNFR_NGFR_1; 1.			
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.			
KW	Receptor.			
FT	NON_TER 1			
FT	SEQUENCE 457 AA; 48120 MW; 18634BB1F15D77AC CRC64;			
Query Match	9.4%; Score 326.5; DB 4; Length 457;			
Best Local Similarity	29.2%; Pred. No. 1.3e-18;			
Matches	103; Conservative 38; Mismatches 125; Indels 87; Ga.			
QY	42 QPEQZASNLIGTYRHVDR--TGQYLTCDKCPA--GTVSEHCTNTSIRVCSSCPV			
Db	23 QPDPAH--GARRRLGAGRRTG-ALGGCARLARPQHQAKVFCTKTSITVCDSCED			
QY	97 TRHENGIEKHDCSQCPWPWPMIEKLPCAAALTDIRECTCPGFMF----OSNATCAH			
Db	80 TQLWMTWPBCLSGCRCSQDVQETOACTREQR CTCRPWYICALSKQEBGCRLLCPA			
QY	151 PVGNGYRKKGKTTEDYRKCKOARGTFSDVPSYSSMKCKAYTDCLSONLYVYKPGTKETI			
Db	140 RPGFGRARPGTETSDPVKCPAGTFSNTSISDICRPHQIC--NVAVL-PGNASMS			
QY	211 CGTLPSSFSSTSP---SPGTAIPRP---ERMETHEVPS---STVPGKMSNS			
Db	196 C-----TGTSPTRSMAPGAVHLFQPVSTRSQTQPTPEPSTAPSTSFLPMGPSP			
QY	257 NSS-----ASVRPKVTLSSIOGTVPD-NTSSAR			
Db	249 GSTGDFALPVLIGVYTAQLLIGVNCVIMQKKPKLQREAKVHLPADKAR			
QY	287 DVNKTLPLNQYVNNHQGQPHRHILKLPSMEATGKSSSTPI--KGPKRCHER			
Db	307 -----TQGPBQHLLTAPSSSSLESASALDRAPTRNQPQ			
RESULT 6	-			
Q9CWT1	PRELIMINARY;	PRT;	285 AA.	
ID	Q9CWT1;			
AC	Q9CWT1;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-JUN-2003 (TREMBLrel. 19, Last sequence update)			
DB	Putative decoy receptor 3 protein.			
OC	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;			

OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.	8.9%; Score 307; DB 13; Length 285;
OX	NCBI_TAXID=8022;	Best Local Similarity 38.4%; Pred. No. 2.7e-17;
RN	[1]	Matches 61; Conservative 20; Mismatches 76; Indels 2; Gaps 1;
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Leukocyte;	
RA	Plegueuelos O.; Seacombe C.J.;	
RT	"Screening a rainbow trout (Oncorhynchus mykiss) cDNA library."	
RL	Submitted (JUN-2001) to the ENBL/GenBank/DBJU databases.	
DR	EMBL: AJ315137; CAC13329; 1;	
GO	GO:0004877; P: receptor activity; IEA.	
DR	InterPro: IPR005209; EGF like.	
DR	InterPro: IPR001368; TNFR_c6.	
DR	Pfam: PF00020; TNFR_c6; 3.	
DR	SMART: SM00186; EGF 2.	
DR	PROSITE: PS00652; TNFR_NGFR_1; 1.	
DR	PROSITE: PS50059; TNFR_NGFR_2; 1.	
RW	Receptor.	
SEQUENCE	285 AA; 31642 MW; FB75CF1C1E391A00 CRC64;	
SQ	Query Match 8.9%; Score 308; DB 13; Length 285;	PRELIMINARY;
	Best Local Similarity 35.6%; Pred. No. 2.3e-17;	PRT; 474 AA.
Matches	67; Conservative 22; Mismatches 79; Indels 20; Gaps 3;	
DR	30 TYRHVDRAATGQVLTCDKCPAGTYVSSHCTNTSLRVYSSCPVGTFRHNGIEKCHDCSQP 112	
Qy	53 TYRHVDRAATGQVLTCDKCPAGTYVSSHCTNTSLRVYSSCPVGTFRHNGIEKCHDCSQP 112	
Db	30 TYRHVDRAATGQVLTCDKCPAGTYVSSHCTNTSLRVYSSCPVGTFRHNGIEKCHDCSQP 112	
Qy	113 CWPWMLKLPICALTDRECTCPPGMFQSNTACAPHTVCPYGVRKKGTETEDYRCKQCA 172	
Db	90 CTADEIBSVPTQHLNRQCEKDGFTNTHGCSRERRCPGEGVTSNGTAHTDVKCEPP 149	
Qy	173 RGTFSDPVSSWVKRAYTDCLSQNLYVTKPCTEDNVCGTLPSPFSSSSPSPSTAIFR 232	
Db	150 VGFSSAVSSRRAKQFSSVCPGGRTI-PNDNDVYC-SACTNGS----- 193	
Qy	233 PHEMTHE 240	
Db	194 ----RTH 197	
RESULT 7	Q90YS6	PRELIMINARY;
ID	Q90YS6	PRT; 285 AA.
AC	AC_0004872; P: receptor activity; IEA.	
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DE	TNF decoy receptor.	
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteiostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Buteiostomi; Oncorhynchus.	
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Liu L., Fujii K., Dixon B., Sundick R.S.;	
RT	"Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine with a fractalkine-like stalk and a TNF decoy receptor using cDNA fragments containing AU-rich elements."	
RL	Submitted (JUL-2001) to the ENBL/GenBank/DBJU databases.	
DR	EMBL: AF401631; AAK91758; 1;	
DR	GO:0004872; P: receptor activity; IEA.	
DR	InterPro: IPR005619; EGF like.	
DR	InterPro: IPR001368; TNFR_c6.	
DR	SMART: SM00208; TNFR_c3.	
DR	PROSITE: PS00652; TNFR_NGFR_1; 1.	
DR	PROSITE: PS50059; TNFR_NGFR_2; 1.	
RW	Receptor.	
SEQUENCE	285 AA; 31795 MW; 5E3BD1B6EFC6BABC CRC64;	
Query Match 8.9%; Score 307; DB 13; Length 285;	Best Local Similarity 38.4%; Pred. No. 2.7e-17;	Matches 61; Conservative 20; Mismatches 76; Indels 2; Gaps 1;
53 TYRHVDRAATGQVLTCDKCPAGTYVSSHCTNTSLRVYSSCPVGTFRHNGIEKCHDCSQP 112	30 TYRHVDRAATGQVLTCDKCPAGTYVSSHCTNTSLRVYSSCPVGTFRHNGIEKCHDCSQP 112	
113 CWPWMLKLPICALTDRECTCPPGMFQSNTACAPHTVCPYGVRKKGTETEDYRCKQCA 172	90 CTADEIBSVPTQHLNRQCEKDGFTNTHGCSRERRCPGEGVTSNGTAHTDVKCEPP 149	
173 RGTFSDPVSSWVKRAYTDCLSQNLYVTKPCTEDNVCGTLPSPFSSSSPSPSTAIFR 232	150 VGFSSAVSSRRAKQFSSVCPGGRTI-PNDNDVYC-SACTNGS----- 193	
RESULT 8	Q90WY6	PRELIMINARY;
ID	Q90WY6	PRT; 474 AA.
AC	Q90WY6;	
DT	01-JUN-2003 (TREMBLrel. 24, Created)	
DT	01-OCT-2003 (TREMBLrel. 24, Last sequence update)	
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DE	Tumor necrosis factor receptor type II.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheroia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OC	NCBI_TaxID=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Wiistar; TISSUE=Spleen;	
RA	Li Y., Ji A., Schaefer M.K.	
RA	Expression of TNFR2 in rat dorsal root ganglion.;	
RL	Submitted (MAR-2002) to the ENBL/GenBank/DBJU databases.	
DR	EMBL: AF490309; AAP33151; 1;	
DR	GO:0004872; P: receptor activity; IEA.	
DR	InterPro: IPR01368; TNFR_c6.	
DR	Pfam: PF00020; TNFR_c6; 4.	
DR	SMART: SM00208; TNFR_c4.	
DR	PROSITE: PS00652; TNFR_NGFR_1; 2.	
DR	PROSITE: PS50059; TNFR_NGFR_2; 3.	
KN	Receptor.	
SEQUENCE	474 AA; 50148 MW; 29866AB9E8C8D714 CRC64;	
Query Match 8.1%; Score 281.5; DB 11; Length 474;	Best Local Similarity 25.9%; Pred. No. 7.9e-15;	Matches 83; Conservative 39; Mismatches 128; Indels 71; Gaps 11;
65 LTCDKCPAGTYVSEHCTNTSLRVYSSCPVGTFRHNGIEKCHDCSQP 124	53 MCCAKCIPGQVAKHFCNKTSDTVCAAGMTQVNHLHTCLSSCSDDQVETHNCT 112	
125 ALTDIRECTCPPMF----OSNA-TCAPIHTVCPYGVRKKGTETEDYRCKQCA 177	173 DTTSSTDVCRPRIC---SILAIPNASIDAVCA---SESPISAVRTIVYQPEP 223	
113 KQONRVCACNADSYCALKIHSGNCRQCMKLSKCGCPFGVARSRTSGNVTCSAGP 172	178 TRSQPMVQEPGTSQTHIPVSLGSLTIEPSITGGSLPGLIVLTLGMLGLANC 283	
Qy	113 KQONRVCACNADSYCALKIHSGNCRQCMKLSKCGCPFGVARSRTSGNVTCSAGP 172	
Db	53 MCCAKCIPGQVAKHFCNKTSDTVCAAGMTQVNHLHTCLSSCSDDQVETHNCT 112	
Qy	173 DTTSSTDVCRPRIC---SILAIPNASIDAVCA---SESPISAVRTIVYQPEP 223	
Db	178 TRSQPMVQEPGTSQTHIPVSLGSLTIEPSITGGSLPGLIVLTLGMLGLANC 283	
Qy	173 DTTSSTDVCRPRIC---SILAIPNASIDAVCA---SESPISAVRTIVYQPEP 223	
Db	178 TRSQPMVQEPGTSQTHIPVSLGSLTIEPSITGGSLPGLIVLTLGMLGLANC 283	
Qy	263 ---RPKVLSSTQEGTVPDNTESSARGKEDVNTKTLPLQVNHNQGPHPHRHLKLP 318	
Db	263 ---RPKVLSSTQEGTVPDNTESSARGKEDVNTKTLPLQVNHNQGPHPHRHLKLP 318	
Qy	319 TGGEKSTT-TIKGPRGHPR 337	
Db	330 SSLESSASAGDRRAPPGHPQ 350	

OX	NCBI_TaxID=10116;	PX	MEDLINE-95178848; PubMed-7873884;
RN	SEQUENCE FROM N.A.	RA	Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RC	STRAIN=Sprague-Dawley.	RT	"Allelic variation of the type 2 tumor necrosis factor receptor gene".
RA	Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;	RL	Gene 5:726-727(1994).
RT	"TNF-receptors p60 and p80 are constitutively expressed by rat brain capillary endothelial cells and participate in TNF-alpha transport through the blood-brain barrier."	DR	Mamm. Genome 5:726-727(1994).
RT	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.	DR	DRB; T48854; 148854.
DR	EMBL: AF42014; AAL16021.1;	DR	HSSP; PI9438; 1NCP.
DR	GO: GO:0004872; F: receptor activity; IEA.	DR	MGP; MG:134483; Thirifib.
DR	InterPro: IPR001368; TNFR_C6.	DR	GO:0007166; P: cell surface receptor linked signal transdu. . .; IMP.
DR	Pfam: PF00020; TNFR_C6.	DR	GO:0006554; P: inflammatory response; IMP.
SMART	SM00208; TNFR_4.	DR	DR InterPro: IPR01368; TNFR_C6.
PROSITE	PS00652; TNFR_NGFR_1;	DR	Pfam: PF00020; TNFR_C6.
PROSITE	PS00500; TNFR_NGFR_2;	DR	SMART; SM00208; TNFR_4.
KW	NON_TER	DR	PROSITE; PS00500; TNFR_NGFR_2; 3.
FT	1	KW	Receptor.
FT	NON_TER	1	NON_TER
SQ	433 AA; 433 MW;	FT	1
SEQUENCE	433 AA;	FT	275-5; DB 11; Length 459;
Db	Score 8.0%; Best Local Similarity 26.1%; Pred. No. 2.2e-14;	FT	8.0%; Score 275-5; DB 11; Length 459;
Db	33 MCCAOKCPGQYAKHFCNKTSDTVCADAGMFTOWNHATCLSSSSSSSDQVETHNCT 92	FT	93 93 T > I.
Qy	125 ALTDRECTCOPGMF----OSNA-TCAHTVCPVGWGRKKGCTEDYTRCKOCARGAT 177	FT	93 93 T > I.
Db	93 KQNRVACNAQDSYCAIKLHSQNCRQMRISKCGFGVRSRSGNTCSAAGPIDS 152	FT	268 268 P > I.
Qy	65 LTCDKCPAGTYVSEHCTNTSLRVCCSVPVGTFTRHENGIEKXCHDQSOPCPWPMBKLPCA 124	FT	345 345 Y > F.
Db	33 MCCAOKCPGQYAKHFCNKTSDTVCADAGMFTOWNHATCLSSSSSSSDQVETHNCT 92	FT	421 421 MW;
Qy	178 DVESSYMKCKAYTDCLSQNLVYKPGTKETDNVCGTLPSPSSSTS- PGTAIFPRP- 234	FT	48686 MW;
Db	153 DTTSSTDVCPRERIC---SILAIPGNSTDAVCA----SESPTPSAVPRTIVSQPP 203	FT	6C51D2C71C4622DF CRC64;
Qy	235 ---AMTHEVDSST-YVKPMNST---ESNSSAV--- 262	FT	6C51D2C71C4622DF CRC64;
Db	204 TRSQPMQEQPSQTQPHIPVSLGSPTIPEPSITGGSLPIGLVGLTLLGLMLGLANC 263	FT	6C51D2C71C4622DF CRC64;
Qy	263 ---RPKVLSSTQEGTPDNTSSARGKDYNKTLPNLQVYNNHQCPHHHLKULPSY 318	FT	6C51D2C71C4622DF CRC64;
Db	264 ILVQRKPKPSQIQLTMYHPDERSQDAV-----GLEQHILLTAPSSS 309	FT	6C51D2C71C4622DF CRC64;
Qy	319 :T:GEGKSSTPIKGPKRGP 336	FT	6C51D2C71C4622DF CRC64;
Db	310 SSLESSAS--AGDRRAPP 325	FT	6C51D2C71C4622DF CRC64;
RESULT 12	Q62327	PRELIMINARY;	PRT; 459 AA.
AC	Q62327	PRELIMINARY;	PRT; 459 AA.
DT	01-OCT-1996 (TREMBLrel. 01, Created)	Q9PUS0	PRELIMINARY;
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	AC	PRT; 302 AA.
DE	Murine tumour necrosis factor receptor 2 protein (Fragment)	Q9PUS0	PRT;
GN	TNFRSF1B.	DT	01-MAY-2000 (TREMBLrel. 13, Created)
OS	Mus musculus (Mouse)	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
OC	NCBI_TaxID=10050;	DE	Decoy TNF receptor.
RN	[1] SEQUENCE FROM N.A.	OS	Salvelinus fontinalis (Brook trout) (Brook char).
RP	RC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Protostanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
RC	SEQUENCE FROM NOD;	OC	NCBI_TaxID=8038;
RA	Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;	RN	SEQUENCE FROM N.A.
RT	"Amino acid variation in the tumor Necrosis factor receptor 2 is linked to autoimmune diabetes in NOD mice.";	RP	SEQUENCE FROM N.A.
RL	Genomics 0:0-0(0).	RX	MEDLINE=2011091; PubMed-10642582;
RN	[2] SEQUENCE FROM N.A.	RA	Bobe J., Goetz F.W.;
RC	SEQUENCE FROM NOD;	RT	"A tumor necrosis factor decoy receptor homologue is up-regulated in

Db	108	NSSRVCEERPGMFCQTAAKNTCMRCQRHTACKPGFVKIRGTCSEIDVSCEECPPOTFSQ	167
Qy	180	PSSVMKCKRAYTDLSQNTLVIKPGTKETDNYC-GTLPSSSSSPGTATIFPRPEHMBT	238
Db	168	SSSTDVCKPHTDCAKLNKVAQGKGNAHDQVCTDQLPSYL----TPDTSSI---RIT	217
Qy	239	HEVPSSSTYVPKMNSTSSNSASVRKVLSSQEGTVPDNTSSARGKEDYNKTLPNL	295
Db	218	NETDDSDVLRNAN-----PVTASLSSATTEI PGSTDDEEALAGTSPTL	263

Search completed: September 21, 2004, 22:44:03
Job time : 133 secs